

Sequence Listing

<110> Baker, Kevin P.
 Botstein, David
 Desnoyers, Luc
 Eaton, Dan L.
 Ferrara, Napoleone
 Fong, Sherman
 Gao, Wei-Qiang
 Goddard, Audrey
 Godowski, Paul J.
 Grimaldi, Christopher J.
 Gurney, Austin L.
 Hillan, Kenneth J.
 Pan, James
 Paoni, Nicholas F.
 Roy, Margaret Ann
 Smith, Victoria
 Stewart, Timothy A.
 Tumas, Daniel
 Watanabe, Colin K.
 Williams, P. Mickey
 Wood, William I.

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 <222> 161-163, 187-190 and 253-256
 <223> N-glycosylation Sites.

<400> 10
 Met Leu Phe Trp Val Leu Gly Leu Leu Ile Leu Cys Gly Phe Leu
 1 5 10 15
 Trp Thr Arg Lys Gly Lys Leu Lys Ile Glu Asp Ile Thr Asp Lys
 20 25 30
 Tyr Ile Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala
 35 40 45
 Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys
 50 55 60
 Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu
 65 70 75
 Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val
 80 85 90
 Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly
 95 100 105
 Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala
 110 115 120
 Pro Thr Asp Trp Leu Thr Leu Glu Asp Tyr Arg Glu Pro Ile Glu
 125 130 135
 Val Asn Leu Phe Gly Leu Ile Ser Val Thr Leu Asn Met Leu Pro
 140 145 150
 Leu Val Lys Lys Ala Gln Gly Arg Val Ile Asn Val Ser Ser Val
 155 160 165
 Gly Gly Arg Leu Ala Ile Val Gly Gly Gly Tyr Thr Pro Ser Lys
 170 175 180
 Tyr Ala Val Glu Gly Phe Asn Asp Ser Leu Arg Arg Asp Met Lys
 185 190 195

Ala	Phe	Gly	Val	His	Val	Ser	Cys	Ile	Glu	Pro	Gly	Leu	Phe	Lys	
				200						205				210	
Thr	Asn	Leu	Ala	Asp	Pro	Val	Lys	Val	Ile	Glu	Lys	Lys	Leu	Ala	
				215						220				225	
Ile	Trp	Glu	Gln	Leu	Ser	Pro	Asp	Ile	Lys	Gln	Gln	Tyr	Gly	Glu	
				230						235				240	
Gly	Tyr	Ile	Glu	Lys	Ser	Leu	Asp	Lys	Leu	Lys	Gly	Asn	Lys	Ser	
				245						250				255	
Tyr	Val	Asn	Met	Asp	Leu	Ser	Pro	Val	Val	Glu	Cys	Met	Asp	His	
				260						265				270	
Ala	Leu	Thr	Ser	Leu	Phe	Pro	Lys	Thr	His	Tyr	Ala	Ala	Gly	Lys	
				275						280				285	
Asp	Ala	Lys	Ile	Phe	Trp	Ile	Pro	Leu	Ser	His	Met	Pro	Ala	Ala	
				290						295				300	
Leu	Gln	Asp	Phe	Leu	Leu	Leu	Lys	Gln	Lys	Ala	Glu	Leu	Ala	Asn	
				305						310				315	
Pro Lys Ala Val															

<210> 11
 <211> 2720
 <212> DNA
 <213> Homo sapiens

<400> 11
 gcgggctggt gacggcgctg cgatggctgc ctgcgagggc aggagaagcg 50
 gagctctcgg ttcctctcag tcggacttcc tgacgccgcc agtgggaggg 100
 gccccttggg ccgtcgccac cactgtagtc atgtaccac cgccgccgcc 150
 gccgcctcat cgggacttca tctcggtgac gctgagcttt ggcgagagct 200
 atgacaacag caagagttgg cggcggcgct cgtgctggag gaaatggaag 250
 caactgtcga gattgcagcg gaatatgatt ctcttctctc ttgcctttct 300
 gcttttctgt ggactcctct totacatcaa cttggctgac cattggaaag 350
 ctctggcttt caggctagag gaagagcaga agatgaggcc agaaattgct 400
 gggttaaaac cagcaaatac acccgcttta ccagctcctc agaaggcgga 450
 caccgaccct gagaacttac ctgagatttc gtcacagaag acacaaagac 500
 acatccagcg gggaccacct cacctgcaga ttagaccccc aagccaagac 550
 ctgaaggatg ggaccagga ggaggccaca aaaaggcaag aagcccctgt 600
 ggatccccgc ccggaaggag atccgcagag gacagtcac agctggaggg 650

gagcgggtgat cgagcctgag cagggcaccg agctcccttc aagaagagca 700
gaagtgccca ccaagcctcc cctgccaccg gccaggacac agggcacacc 750
agtgcattctg aactatcgcc agaagggcgt gattgacgtc ttcttgcattg 800
catggaaagg ataccgcaag tttgcatggg gccatgacga gctgaagcct 850
gtgtccaggt ccttcagtga gtgggtttggc ctgggtctca cactgatcga 900
cgcgctggac accatgtgga tcttgggtct gaggaagaa tttgaggaag 950
ccaggaagtg ggtgtcgaag aagttacact ttgaaaagga cgtggacgtc 1000
aacctgtttg agagcacgat ccgcattcctg ggggggctcc tgagtgccta 1050
ccacctgtct ggggacagcc tottcttgag gaaagctgag gatttttgaa 1100
atcggctaata gcctgccttc agaacacat ccaagattcc ttactcggat 1150
gtgaacatcg gtactggagt tgcccaccog ccacgggtgga cctccgacag 1200
cactgtggcc gaggtgacca gcattcagct ggagttccgg gagctctccc 1250
gtctcacagg ggataagaag tttcaggagg cagtggagaa ggtgacacag 1300
cacatccacg gcctgtctgg gaagaaggat gggctgggtgc ccatgttcat 1350
caatacccac agtggcctct tcacccacct gggcgtattc acgctgggag 1400
ccagggccga cagctactat gagtacctgc tgaagcagtg gatccagggc 1450
gggaagcagg agacacagct gctggaagac tacgtggaag ccatcgaggg 1500
tgtcagaacg cacctgctgc ggcactccga gccagtaag ctacactttg 1550
tgggggagct tgcccacggc cgcttcagtg ccaagatgga ccacctggtg 1600
tgcttcctgc cagggacgct ggctctgggc gtctaccacg gcctgcccgc 1650
cagccacatg gagctggccc aggagctcat ggagacttgt taccagatga 1700
accggcagat ggagacgggg ctgagtcocg agatcgtgca cttcaacctt 1750
tacccccagc cgggcccgtc ggacgtggag gtcaagccag cagacaggca 1800
caacctgctg cggccagaga ccgtggagag cctgttctac ctgtaccgcg 1850
tcacagggga ccgcaaatac caggactggg gctgggagat tctgcagagc 1900
ttcagccgat tcacacgggt cccctcgggt ggctattctt ccatcaacaa 1950
tgtccaggat cctcagaagc ccgagcctag ggacaagatg gagagcttct 2000
tcctggggga gacgtcaag tatctgttct tgctcttctc cgatgacca 2050
aacctgctca gcctggacgc ctacgtgttc aacaccgaag cccaccctct 2100

gcctatctgg acccctgcct aggggtggatg gctgctggtg tggggacttc 2150
 ggggtgggcag aggcaccttg ctgggtctgt ggcattttcc aaggggccac 2200
 gtagcaccgg caaccgcaa gtggcccagg ctctgaactg gctctgggct 2250
 cctcctcgtc tctgctttaa tcaggacacc gtgaggacaa gtgaggccgt 2300
 cagtcttggt gtgatgcggg gtgggctggg ccgctggagc ctccgcctgc 2350
 ttcctccaga agacacgaat catgactcac gattgctgaa gcctgagcag 2400
 gtctctgtgg gccgaccaga ggggggcttc gaggtggtcc ctggtactgg 2450
 ggtgaccgag tggacagccc aggggtgcagc tctgcccggg ctctggaagc 2500
 ctcatgctc cccaatccaa gggctctggag gggctgccgt gactccagag 2550
 gcctgaggct ccagggtctg ctctggtggt tacaagctgg actcagggat 2600
 cctcctggcc gcccgcagg gggcttggag ggctggacgg caagtccgtc 2650
 tagctcacgg gcccctccag tggaatgggt cttttcgggt gagataaaag 2700
 ttgatttgct ctaaccgcaa 2720

<210> 12
 <211> 699
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> TRANSMEM
 <222> 21-40 and 84-105
 <223> Transmembrane Domain (type II)

<400> 12
 Met Ala Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser
 1 5 10 15
 Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala
 20 25 30
 Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro
 35 40 45
 His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr
 50 55 60
 Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp
 65 70 75
 Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu
 80 85 90
 Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala
 95 100 105

Asp	His	Trp	Lys	Ala	Leu	Ala	Phe	Arg	Leu	Glu	Glu	Glu	Gln	Lys		110	115	120
Met	Arg	Pro	Glu	Ile	Ala	Gly	Leu	Lys	Pro	Ala	Asn	Pro	Pro	Val		125	130	135
Leu	Pro	Ala	Pro	Gln	Lys	Ala	Asp	Thr	Asp	Pro	Glu	Asn	Leu	Pro		140	145	150
Glu	Ile	Ser	Ser	Gln	Lys	Thr	Gln	Arg	His	Ile	Gln	Arg	Gly	Pro		155	160	165
Pro	His	Leu	Gln	Ile	Arg	Pro	Pro	Ser	Gln	Asp	Leu	Lys	Asp	Gly		170	175	180
Thr	Gln	Glu	Glu	Ala	Thr	Lys	Arg	Gln	Glu	Ala	Pro	Val	Asp	Pro		185	190	195
Arg	Pro	Glu	Gly	Asp	Pro	Gln	Arg	Thr	Val	Ile	Ser	Trp	Arg	Gly		200	205	210
Ala	Val	Ile	Glu	Pro	Glu	Gln	Gly	Thr	Glu	Leu	Pro	Ser	Arg	Arg		215	220	225
Ala	Glu	Val	Pro	Thr	Lys	Pro	Pro	Leu	Pro	Pro	Ala	Arg	Thr	Gln		230	235	240
Gly	Thr	Pro	Val	His	Leu	Asn	Tyr	Arg	Gln	Lys	Gly	Val	Ile	Asp		245	250	255
Val	Phe	Leu	His	Ala	Trp	Lys	Gly	Tyr	Arg	Lys	Phe	Ala	Trp	Gly		260	265	270
His	Asp	Glu	Leu	Lys	Pro	Val	Ser	Arg	Ser	Phe	Ser	Glu	Trp	Phe		275	280	285
Gly	Leu	Gly	Leu	Thr	Leu	Ile	Asp	Ala	Leu	Asp	Thr	Met	Trp	Ile		290	295	300
Leu	Gly	Leu	Arg	Lys	Glu	Phe	Glu	Glu	Ala	Arg	Lys	Trp	Val	Ser		305	310	315
Lys	Lys	Leu	His	Phe	Glu	Lys	Asp	Val	Asp	Val	Asn	Leu	Phe	Glu		320	325	330
Ser	Thr	Ile	Arg	Ile	Leu	Gly	Gly	Leu	Leu	Ser	Ala	Tyr	His	Leu		335	340	345
Ser	Gly	Asp	Ser	Leu	Phe	Leu	Arg	Lys	Ala	Glu	Asp	Phe	Gly	Asn		350	355	360
Arg	Leu	Met	Pro	Ala	Phe	Arg	Thr	Pro	Ser	Lys	Ile	Pro	Tyr	Ser		365	370	375
Asp	Val	Asn	Ile	Gly	Thr	Gly	Val	Ala	His	Pro	Pro	Arg	Trp	Thr		380	385	390
Ser	Asp	Ser	Thr	Val	Ala	Glu	Val	Thr	Ser	Ile	Gln	Leu	Glu	Phe				

	395		400		405
Arg Glu Leu Ser	Arg Leu Thr Gly Asp	Lys Lys Phe Gln Glu Ala			
	410	415			420
Val Glu Lys Val	Thr Gln His Ile His	Gly Leu Ser Gly Lys Lys			
	425	430			435
Asp Gly Leu Val	Pro Met Phe Ile Asn	Thr His Ser Gly Leu Phe			
	440	445			450
Thr His Leu Gly	Val Phe Thr Leu Gly	Ala Arg Ala Asp Ser Tyr			
	455	460			465
Tyr Glu Tyr Leu	Leu Lys Gln Trp Ile	Gln Gly Gly Lys Gln Glu			
	470	475			480
Thr Gln Leu Leu	Glu Asp Tyr Val Glu	Ala Ile Glu Gly Val Arg			
	485	490			495
Thr His Leu Leu	Arg His Ser Glu Pro	Ser Lys Leu Thr Phe Val			
	500	505			510
Gly Glu Leu Ala	His Gly Arg Phe Ser	Ala Lys Met Asp His Leu			
	515	520			525
Val Cys Phe Leu	Pro Gly Thr Leu Ala	Leu Gly Val Tyr His Gly			
	530	535			540
Leu Pro Ala Ser	His Met Glu Leu Ala	Gln Glu Leu Met Glu Thr			
	545	550			555
Cys Tyr Gln Met	Asn Arg Gln Met Glu	Thr Gly Leu Ser Pro Glu			
	560	565			570
Ile Val His Phe	Asn Leu Tyr Pro Gln	Pro Gly Arg Arg Asp Val			
	575	580			585
Glu Val Lys Pro	Ala Asp Arg His Asn	Leu Leu Arg Pro Glu Thr			
	590	595			600
Val Glu Ser Leu	Phe Tyr Leu Tyr Arg	Val Thr Gly Asp Arg Lys			
	605	610			615
Tyr Gln Asp Trp	Gly Trp Glu Ile Leu	Gln Ser Phe Ser Arg Phe			
	620	625			630
Thr Arg Val Pro	Ser Gly Gly Tyr Ser	Ser Ile Asn Asn Val Gln			
	635	640			645
Asp Pro Gln Lys	Pro Glu Pro Arg Asp	Lys Met Glu Ser Phe Phe			
	650	655			660
Leu Gly Glu Thr	Leu Lys Tyr Leu Phe	Leu Leu Phe Ser Asp Asp			
	665	670			675
Pro Asn Leu Leu	Ser Leu Asp Ala Tyr	Val Phe Asn Thr Glu Ala			
	680	685			690

His Pro Leu Pro Ile Trp Thr Pro Ala
695

<210> 13
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 13
cgccagaagg gcgtgattga cgtc 24

<210> 14
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 14
ccatccttct tcccagacag gccg 24

<210> 15
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 15
gaagcctgtg tccaggctct tcagtgaagt gtttggcctc ggtc 44

<210> 16
<211> 1524
<212> DNA
<213> Homo sapiens

<400> 16
ggcgccgcgt aggcccgga ggccgggccg gccgggctgc gagcgctgc 50
cccatgcgcc gccgcctctc cgcacgatgt tcccctcgcg gaggaaagcg 100
gcgcagctgc cctgggagga cggcaggtcc gggttgctct ccggcgccct 150
ccctcggaag tgttccgtct tccacctgtt cgtggcctgc ctctcgctgg 200
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

cgggcagtca ggggacaagg gcaggagacc tcgggccctc cccgtgcctg 300
 cccccagag ccgccccctg agcactggga agaagacgca tcctggggcc 350
 cccaccgcct ggcagtgtg gtgcccttcc gcgaacgctt cgaggagctc 400
 ctggttcttcg tgccccacat gcgccgcttc ctgagcagga agaagatccg 450
 gcaccacatc tacgtgtctca accaggtgga ccacttcagg ttcaaccggg 500
 cagcgctcat caacgtgggc ttcttgga gaagcaacag caccgactac 550
 attgccatgc acgacgttga cctgtctcct ctcaacgagg agctggacta 600
 tggctttcct gaggctgggc ccttcacgt ggctccccg gagctccacc 650
 ctctctacca ctacaagacc tatgtcggcg gcatcctgct gctctccaag 700
 cagcactacc ggctgtgcaa tgggatgtcc aaccgcttct ggggctgggg 750
 ccgcgaggac gacgagttct accggcgcat taaggagct gggctccagc 800
 ttttcgccc ctcggaatc acaactgggt acaagacatt tcgccacctg 850
 catgaccag cctggcgga gagggaccag aagcgcatcg cagctcaaaa 900
 acaggagcag ttcaaggtgg acagggagg aggcctgaac actgtgaagt 950
 accatgtggc ttccgcact gccctgtctg tgggcggggc cccctgcact 1000
 gtctcaaca tcatgttga ctgtgacaag accgccacac cctggtgcac 1050
 attcagctga gctggatga cagtaggaa gcctgtacct acaggccata 1100
 ttgctcaggc tcaggacaag gcctcaggtc gtgggccag ctctgacagg 1150
 atgtggagtg gccaggacca agacagcaag ctacgcaatt gcagccacc 1200
 ggccgccaag gcaggcttgg gctgggccag gacacgtggg gtgcctggga 1250
 cgctgcttgc catgcacagt gatcagagag aggcctgggt gtgtcctgtc 1300
 cgggaccccc cctgccttcc tgctcaccct actctgacct ccttcacgtg 1350
 cccaggcctg tgggtagtgg ggagggtga acaggacaac ctctcatcac 1400
 cctactctga cctccttcac gtgccaggc ctgtgggtag tggggagggc 1450
 tgaacaggac aacctctcat ccccccaaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17
 <211> 327
 <212> PRT
 <213> Homo sapiens
 <220>

<221> sig_peptide
 <222> 1-42
 <223> Signal peptide.

 <220>
 <221> misc_feature
 <222> 19-25,65-71,247-253,285-291,303-310
 <223> N-myristoylation site.

 <220>
 <221> misc_feature
 <222> 27-31
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

 <220>
 <221> TRANSMEM
 <222> 29-49
 <223> Transmembrane domain (type II).

 <220>
 <221> misc_feature
 <222> 154-158
 <223> N-glycosylation site.

 <220>
 <221> misc_feature
 <222> 226-233
 <223> Tyrosine kinase phosphorylation site.

<400> 17
 Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp
 1 5 10 15
 Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser
 20 25 30
 Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser
 35 40 45
 Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala
 50 55 60
 Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys
 65 70 75
 Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp
 80 85 90
 Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe
 95 100 105
 Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser
 110 115 120
 Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp
 125 130 135
 His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

	140		145		150
Glu Ser Ser Asn Ser Thr Asp Tyr Ile	Ala Met His Asp Val Asp				
	155		160		165
Leu Leu Pro Leu Asn Glu Glu Leu Asp	Tyr Gly Phe Pro Glu Ala				
	170		175		180
Gly Pro Phe His Val Ala Ser Pro Glu	Leu His Pro Leu Tyr His				
	185		190		195
Tyr Lys Thr Tyr Val Gly Gly Ile Leu	Leu Leu Ser Lys Gln His				
	200		205		210
Tyr Arg Leu Cys Asn Gly Met Ser Asn	Arg Phe Trp Gly Trp Gly				
	215		220		225
Arg Glu Asp Asp Glu Phe Tyr Arg Arg	Ile Lys Gly Ala Gly Leu				
	230		235		240
Gln Leu Phe Arg Pro Ser Gly Ile Thr	Thr Gly Tyr Lys Thr Phe				
	245		250		255
Arg His Leu His Asp Pro Ala Trp Arg	Lys Arg Asp Gln Lys Arg				
	260		265		270
Ile Ala Ala Gln Lys Gln Glu Gln Phe	Lys Val Asp Arg Glu Gly				
	275		280		285
Gly Leu Asn Thr Val Lys Tyr His Val	Ala Ser Arg Thr Ala Leu				
	290		295		300
Ser Val Gly Gly Ala Pro Cys Thr Val	Leu Asn Ile Met Leu Asp				
	305		310		315
Cys Asp Lys Thr Ala Thr Pro Trp Cys	Thr Phe Ser				
	320		325		

<210> 18
 <211> 23
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

 <400> 18
 gcgaacgctt cgaggagtcc tgg 23

 <210> 19
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence

<222> 1-24
 <223> Synthetic construct
 <400> 19
 gcagtgcggg aagccacatg gtac 24

<210> 20
 <211> 46
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-46
 <223> Synthetic construct.

<400> 20
 cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21
 <211> 494
 <212> DNA
 <213> Homo sapiens

<400> 21
 caatgtttgc ctatccacct cccccaagcc cctttaccta tgctgctgct 50
 aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100
 gactggtcgg tgcccagaaa gtctcttctg ccactgacgc ccccatcagg 150
 gattgggcct tctttccccc ttcttttctg tgtctcctgc ctcatcggcc 200
 tgccatgacc tgcagccaag ccagcccccg tggggaaggg gagaaagtgg 250
 gggatggcta agaaagctgg gagatagga acagaagagg gtagtgggtg 300
 ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350
 atttatacaa agatattaag gcctgtttca ttaagaaatt gttcccttcc 400
 cctgtgttca atgtttgtaa agattgttct gtgtaaatat gtctttataa 450
 taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22
 <211> 73
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-15
 <223> Signal peptide.

<220>
 <221> misc_feature
 <222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Leu Lys Gly
1 5 10 15

Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
20 25 30

Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
35 40 45

Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
50 55 60

Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
65 70

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

gggacccatg cggccgtgac ccccggtcc ctagaggccc agcgcagccg 50

cagcggacaa aggagcatgt ccgcgccggg gaaggcccgt cctccggccg 100

ccataaggct ccggtcgccg ctgggcccgc gccgcgctcc tgcccggccg 150

ggctccgggg cggcccgtta ggccagtgcg ccgcgcgtcg cccgcagggc 200

cccggcccgc agcatggagc caccgggacg ccggcggggc cgcgcgcagc 250

cgccgctgtt gctgccgtc tcgctgttag cgctgctgcg gctgctggga 300

ggcggcgggc gcggcgggc cgcgcgctg cccgcgggt gcaagcacga 350

tgggcggccc cgaggggctg gcagggcggc gggcgccgcc gagggcaagg 400

tgggtgtgag cagcctggaa ctgcgcagc tcctgcccc agatactctg 450

ccaaccgca cggtcaccct gattctgagt aacaataaga tatccgagct 500

gaagaatggc tcattttctg ggttaagtct ccttgaaaga ttggacctcc 550

gaaacaatct tattagtagt atagatccag gtgccttctg gggactgtca 600

tctctaaaaa gattgatct gacaaacaat cgaataggat gtctgaatgc 650

agacatattt cgaggactca ccaatctggg tcggctaaac ctttcgggga 700

atttgttttc ttcattatct caaggaactt ttgattatct tgcgtcatta 750

cggctctttg aattccagac tgagtatctt ttgtgtgact gtaacatact 800

gtggatgcat cgctgggtaa aggagaagaa catcacggtc cgggatacca 850

ggtgtgttta tcctaagtca ctgcaggccc aaccagtcac aggcgtgaag 900
 caggagctgt tgacatgcga cctccgctt gaattgcgtt ctttctacat 950
 gactccatct catcgccaag ttgtgtttga aggagacagc cttcctttcc 1000
 agtgcattggc ttcatatatt gatcaggaca tgcaagtgtt gtggtatcag 1050
 gatgggagaa tagttgaaac cgatgaatcg caaggtattt ttgttgaaaa 1100
 gaacatgatt cacaactgct ccttgattgc aagtgccta accatttcta 1150
 atattcaggc tggatctact ggaaattggg gctgtcatgt ccagacccaa 1200
 cgtgggaata atacgaggac tgtggatatt gtggtattag agagttctgc 1250
 acagtactgt cctccagaga ggggtgtaaa caacaaagggt gacttcagat 1300
 ggcccagaac attggcaggc attactgcat atctgcagtg tacgcggaac 1350
 acccatggca gtgggatata tcccggaaac ccacaggatg agagaaaagc 1400
 ttggcgcaga tgtgatagag gtggcttttg ggcagatgat gattattctc 1450
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 <212> PRT
 <213> Homo sapiens

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 <221> sig_peptide
 <222> 1-33
 <223> Signal peptide.

<220>
 <221> TRANSMEM
 <222> 13-40
 <223> Transmembrane domain (type II).

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 35 40 45
 Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu
 50 55 60
 Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro
 65 70 75
 Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn
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Asn	Lys	Ile	Ser	Glu	Leu	Lys	Asn	Gly	Ser	Phe	Ser	Gly	Leu	Ser	
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				110					115					120	
Asp	Pro	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Ser	Leu	Lys	Arg	Leu	Asp	
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Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg	
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Gly	Leu	Thr	Asn	Leu	Val	Arg	Leu	Asn	Leu	Ser	Gly	Asn	Leu	Phe	
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Ser	Ser	Leu	Ser	Gln	Gly	Thr	Phe	Asp	Tyr	Leu	Ala	Ser	Leu	Arg	
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Ser	Leu	Glu	Phe	Gln	Thr	Glu	Tyr	Leu	Leu	Cys	Asp	Cys	Asn	Ile	
				185					190					195	
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 <222> 1-24

<223> Synthetic construct

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<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

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<222> 1-24

<223> Synthetic construct.

<400> 26

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<210> 27

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 27

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<210> 28

<211> 683

<212> DNA

<213> Homo sapiens

<400> 28

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 <213> Homo sapiens

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 <222> 1-21
 <223> Signal peptide.

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 35 40 45
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 <212> DNA
 <213> Homo sapiens

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 <211> 322
 <212> PRT
 <213> Homo sapiens

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 Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys
 65 70 75
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 80 85 90
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 95 100 105
 Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr
 110 115 120
 Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp
 125 130 135
 His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala
 140 145 150
 Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile
 155 160 165
 Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu
 170 175 180
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 185 190 195
 Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr
 200 205 210

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Val	Leu	Trp	Pro	Leu	Tyr	Gln	Phe	Asp	Glu	Lys	Tyr	Gly	Gly	Gln	
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Pro	Arg	Arg	Ser	Arg	Asp	Val	Ser	Cys	Ser	Arg	Ser	His	Ala	Tyr	
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Tyr	Val	Cys	Ala	Trp	Asp	Arg	Arg	Leu	Ala	Val	Ala	Ile	Leu	Thr	
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<210> 32

<211> 3680

<212> DNA

<213> Homo sapiens

<400> 32

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<210> 33

<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

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Phe Gly Thr Val Ser Cys Glu Tyr Met Leu Gly Ser Pro Leu Ser
20 25 30

Ser Leu Ala Gln Val Asn Leu Ser Pro Phe Ser His Pro Lys Val
35 40 45

His Met Asp Pro Asn Tyr Cys His Pro Ser Thr Ser Leu His Leu
50 55 60

Cys Ser Leu Ala Trp Ser Phe Thr Arg Leu Leu His Pro Pro Leu
65 70 75

Ser Pro Gly Ile Ser Gln Val Val Lys Asp His Val Thr Lys Pro
80 85 90

Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile Glu Trp Lys
95 100 105

Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu Ser Ala
110 115 120

Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg
125 130 135

Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys
140 145 150

Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp
155 160 165

Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala
170 175 180

Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly
185 190 195

His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu
200 205 210

Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser
215 220 225

Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu
230 235 240

Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro
245 250 255

Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala
260 265 270

Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser
275 280 285

Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu
290 295 300

Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser
305 310 315

Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala
320 325 330

Glu Pro Glu Glu Gln
335

<210> 34

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct

<400> 34

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<210> 35

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 35

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<210> 36

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 36

ttccactcaa tgaggtgagc cactc 25

<210> 37

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-23

<223> Synthetic construct.

<400> 37

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<210> 38

<211> 39

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-39

<223> Synthetic construct.

<400> 38

ggagatcgct gcgctggcca ggtcctccct gcatggtat 39

<210> 39

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-22

<223> Synthetic construct.

<400> 39

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<210> 40

<211> 2084

<212> DNA

<213> Homo sapiens

<400> 40

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<210> 41

<211> 334

<212> PRT

<213> Homo sapiens

<400> 41

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Ser	Leu	Leu	Ser	Gly	Ser	His	Gly	Lys	Glu	Asn	Gln	Asp	Ile	Asn
				20					25					30
Thr	Thr	Gln	Asn	Ile	Ala	Glu	Val	Phe	Lys	Thr	Met	Glu	Asn	Lys
				35					40					45
Pro	Ile	Ser	Leu	Glu	Ser	Glu	Ala	Asn	Leu	Asn	Ser	Asp	Lys	Glu
				50					55					60
Asn	Ile	Thr	Thr	Ser	Asn	Leu	Lys	Ala	Ser	His	Ser	Pro	Pro	Leu
				65					70					75
Asn	Leu	Pro	Asn	Asn	Ser	His	Gly	Ile	Thr	Asp	Phe	Ser	Ser	Asn
				80					85					90
Ser	Ser	Ala	Glu	His	Ser	Leu	Gly	Ser	Leu	Lys	Pro	Thr	Ser	Thr
				95					100					105
Ile	Ser	Thr	Ser	Pro	Pro	Leu	Ile	His	Ser	Phe	Val	Ser	Lys	Val
				110					115					120
Pro	Trp	Asn	Ala	Pro	Ile	Ala	Asp	Glu	Asp	Leu	Leu	Pro	Ile	Ser
				125					130					135
Ala	His	Pro	Asn	Ala	Thr	Pro	Ala	Leu	Ser	Ser	Glu	Asn	Phe	Thr
				140					145					150
Trp	Ser	Leu	Val	Asn	Asp	Thr	Val	Lys	Thr	Pro	Asp	Asn	Ser	Ser
				155					160					165
Ile	Thr	Val	Ser	Ile	Leu	Ser	Ser	Glu	Pro	Thr	Ser	Pro	Ser	Val
				170					175					180
Thr	Pro	Leu	Ile	Val	Glu	Pro	Ser	Gly	Trp	Leu	Thr	Thr	Asn	Ser
				185					190					195

Asp	Ser	Phe	Thr	Gly	Phe	Thr	Pro	Tyr	Gln	Glu	Lys	Thr	Thr	Leu
				200					205					210
Gln	Pro	Thr	Leu	Lys	Phe	Thr	Asn	Asn	Ser	Lys	Leu	Phe	Pro	Asn
				215					220					225
Thr	Ser	Asp	Pro	Gln	Lys	Glu	Asn	Arg	Asn	Thr	Gly	Ile	Val	Phe
				230					235					240
Gly	Ala	Ile	Leu	Gly	Ala	Ile	Leu	Gly	Val	Ser	Leu	Leu	Thr	Leu
				245					250					255
Val	Gly	Tyr	Leu	Leu	Cys	Gly	Lys	Arg	Lys	Thr	Asp	Ser	Phe	Ser
				260					265					270
His	Arg	Arg	Leu	Tyr	Asp	Asp	Arg	Asn	Glu	Pro	Val	Leu	Arg	Leu
				275					280					285
Asp	Asn	Ala	Pro	Glu	Pro	Tyr	Asp	Val	Ser	Phe	Gly	Asn	Ser	Ser
				290					295					300
Tyr	Tyr	Asn	Pro	Thr	Leu	Asn	Asp	Ser	Ala	Met	Pro	Glu	Ser	Glu
				305					310					315
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Arg Thr Ser Val														

<210> 42

<211> 1594

<212> DNA

<213> Homo sapiens

<400> 42

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<210> 43
<211> 263
<212> PRT
<213> Homo sapiens

<400> 43
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Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu
35 40 45
Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

	50		55		60
Ser Phe Ile Leu	Ala Gly Leu Ile Val	Gly Gly Ala Cys Ile Tyr			
	65	70			75
Lys Tyr Phe Met	Pro Lys Ser Thr Ile	Tyr Arg Gly Glu Met Cys			
	80	85			90
Phe Phe Asp Ser	Glu Asp Pro Ala Asn	Ser Leu Arg Gly Gly Glu			
	95	100			105
Pro Asn Phe Leu	Pro Val Thr Glu Glu	Ala Asp Ile Arg Glu Asp			
	110	115			120
Asp Asn Ile Ala	Ile Ile Asp Val Pro	Val Pro Ser Phe Ser Asp			
	125	130			135
Ser Asp Pro Ala	Ala Ile Ile His Asp	Phe Glu Lys Gly Met Thr			
	140	145			150
Ala Tyr Leu Asp	Leu Leu Leu Gly Asn	Cys Tyr Leu Met Pro Leu			
	155	160			165
Asn Thr Ser Ile	Val Met Pro Pro Lys	Asn Leu Val Glu Leu Phe			
	170	175			180
Gly Lys Leu Ala	Ser Gly Arg Tyr Leu	Pro Gln Thr Tyr Val Val			
	185	190			195
Arg Glu Asp Leu	Val Ala Val Glu Glu	Ile Arg Asp Val Ser Asn			
	200	205			210
Leu Gly Ile Phe	Ile Tyr Gln Leu Cys	Asn Asn Arg Lys Ser Phe			
	215	220			225
Arg Leu Arg Arg	Arg Asp Leu Leu Leu	Gly Phe Asn Lys Arg Ala			
	230	235			240
Ile Asp Lys Cys	Trp Lys Ile Arg His	Phe Pro Asn Glu Phe Ile			
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Val Glu Thr Lys	Ile Cys Gln Glu				
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<210> 44
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 44
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 <210> 45

<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-20
<223> Synthetic construct.

<400> 45
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<210> 46
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 46
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<210> 47
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-28
<223> Synthetic construct.

<400> 47
cttctcgaac cacataagtt tgaggcag 28

<210> 48
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 48
cacgattccc tccacagcaa ctggg 25

<210> 49
<211> 1969
<212> DNA
<213> Homo sapiens

<400> 49
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 attccggcct gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1950
 aaaaaaaaaa aaaaaaaga 1969

<210> 50
 <211> 283
 <212> PRT
 <213> Homo sapiens

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 20 25 30
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 35 40 45
 Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro
 50 55 60
 Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly
 65 70 75
 Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe
 80 85 90
 Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala
 95 100 105
 Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln
 110 115 120
 Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys
 125 130 135
 Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe
 140 145 150
 Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala
 155 160 165

Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile	Leu	Ala	Ala	Thr	
				170					175					180	
Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly	Gly	Gly	Asp	
				185					190					195	
Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu	Glu	Lys	
				200					205					210	
Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val	Pro	
				215					220					225	
Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu	
				230					235					240	
Glu	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly	
				245					250					255	
Ser	Leu	Leu	Leu	Ala	Gln	Glu	Ala	Gln	Gly	Pro	Val	Gly	Pro	Pro	
				260					265					270	
Glu	Ser	Pro	Cys	Ala	Cys	Ser	Ser	Val	His	Pro	Ser	Val			
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<210> 51

<211> 1734

<212> DNA

<213> Homo sapiens

<400> 51

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cctggcctgc ctctgctgg ccctctgcct gggcagtggg gaggctggcc 250
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ccttgagggc cagggccagg gcaatcctgg aggtctgggg actccgtggg 700

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Ala Ala Asp Ala	Leu 95	Gly Asn Arg Val	Gly 100	Glu Ala Ala His	Ala 105
Leu Gly Asn Thr	Gly 110	His Glu Ile Gly	Arg 115	Gln Ala Glu Asp	Val 120
Ile Arg His Gly	Ala 125	Asp Ala Val Arg	Gly 130	Ser Trp Gln Gly	Val 135
Pro Gly His Ser	Gly 140	Ala Trp Glu Thr	Ser 145	Gly Gly His Gly	Ile 150
Phe Gly Ser Gln	Gly 155	Gly Leu Gly Gly	Gln 160	Gly Gln Gly Asn	Pro 165
Gly Gly Leu Gly	Thr 170	Pro Trp Val His	Gly 175	Tyr Pro Gly Asn	Ser 180
Ala Gly Ser Phe	Gly 185	Met Asn Pro Gln	Gly 190	Ala Pro Trp Gly	Gln 195
Gly Gly Asn Gly	Gly 200	Pro Pro Asn Phe	Gly 205	Thr Asn Thr Gln	Gly 210
Ala Val Ala Gln	Pro 215	Gly Tyr Gly Ser	Val 220	Arg Ala Ser Asn	Gln 225
Asn Glu Gly Cys	Thr 230	Asn Pro Pro Pro	Ser 235	Gly Ser Gly Gly	Gly 240
Ser Ser Asn Ser	Gly 245	Gly Gly Ser Gly	Ser 250	Gln Ser Gly Ser	Ser 255
Gly Ser Gly Ser	Asn 260	Gly Asp Asn Asn	Asn 265	Gly Ser Ser Ser	Gly 270
Gly Ser Ser Ser	Gly 275	Ser Ser Ser Gly	Ser 280	Ser Ser Gly Gly	Ser 285
Ser Gly Gly Ser	Ser 290	Gly Gly Ser Ser	Gly 295	Asn Ser Gly Gly	Ser 300
Arg Gly Asp Ser	Gly 305	Ser Glu Ser Ser	Trp 310	Gly Ser Ser Thr	Gly 315
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Lys Pro Gly Cys	Glu 335	Lys Pro Gly Asn	Glu 340	Ala Arg Gly Ser	Gly 345

Glu	Ser	Gly	Ile	Gln	Gly	Phe	Arg	Gly	Gln	Gly	Val	Ser	Ser	Asn	
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Met	Arg	Glu	Ile	Ser	Lys	Glu	Gly	Asn	Arg	Leu	Leu	Gly	Gly	Ser	
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Gly	Asp	Asn	Tyr	Arg	Gly	Gln	Gly	Ser	Ser	Trp	Gly	Ser	Gly	Gly	
				380					385					390	
Gly	Asp	Ala	Val	Gly	Gly	Val	Asn	Thr	Val	Asn	Ser	Glu	Thr	Ser	
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Pro	Gly	Met	Phe	Asn	Phe	Asp	Thr	Phe	Trp	Lys	Asn	Phe	Lys	Ser	
				410					415					420	
Lys	Leu	Gly	Phe	Ile	Asn	Trp	Asp	Ala	Ile	Asn	Lys	Asp	Gln	Arg	
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 <213> Homo sapiens

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<210> 54
 <211> 280
 <212> PRT
 <213> Homo sapiens

<400> 54

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Glu	Gly	Pro	Ser	Tyr	Ala	Phe	Glu	Val	Asp	Thr	Val	Ala	Pro	Glu
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His	Gly	Leu	Asp	Asn	Ala	Pro	Val	Val	Asp	Gln	Gln	Leu	Leu	Tyr
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Thr	Cys	Cys	Pro	Tyr	Ile	Gly	Glu	Leu	Arg	Lys	Leu	Leu	Ala	Ser
				65					70					75
Trp	Val	Ser	Gly	Ser	Ser	Gly	Arg	Ser	Gly	Gly	Phe	Met	Arg	Lys
				80					85					90
Ile	Thr	Pro	Thr	Thr	Thr	Thr	Ser	Leu	Gly	Ala	Gln	Pro	Ser	Gln
				95					100					105
Thr	Ser	Gln	Gly	Leu	Gln	Ala	Gln	Leu	Ala	Gln	Ala	Phe	Phe	His
				110					115					120
Asn	Gln	Pro	Pro	Ser	Leu	Arg	Arg	Thr	Val	Glu	Phe	Val	Ala	Glu
				125					130					135
Arg	Ile	Gly	Ser	Asn	Cys	Val	Lys	His	Ile	Lys	Ala	Thr	Leu	Val
				140					145					150
Ala	Asp	Leu	Val	Arg	Gln	Ala	Glu	Ser	Leu	Leu	Gln	Glu	Gln	Leu
				155					160					165
Val	Thr	Gln	Gly	Glu	Glu	Gly	Gly	Asp	Pro	Ala	Gln	Leu	Leu	Glu
				170					175					180
Ile	Leu	Cys	Ser	Gln	Leu	Cys	Pro	His	Gly	Ala	Gln	Ala	Leu	Ala
				185					190					195
Leu	Gly	Arg	Glu	Phe	Cys	Gln	Arg	Lys	Ser	Pro	Gly	Ala	Val	Arg
				200					205					210
Ala	Leu	Leu	Pro	Glu	Glu	Thr	Pro	Ala	Ala	Val	Leu	Ser	Ser	Ala
				215					220					225
Glu	Asn	Ile	Ala	Val	Gly	Leu	Ala	Thr	Glu	Lys	Ala	Cys	Ala	Trp
				230					235					240
Leu	Ser	Ala	Asn	Ile	Thr	Ala	Leu	Ile	Arg	Arg	Glu	Val	Lys	Ala
				245					250					255
Ala	Val	Ser	Arg	Thr	Leu	Arg	Ala	Gln	Gly	Pro	Glu	Pro	Ala	Ala
				260					265					270
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<210> 55
<211> 2401
<212> DNA
<213> Homo sapiens

<400> 55

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<210> 56

<211> 299

<212> PRT

<213> Homo sapiens

<400> 56

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				20					25					30

Asn	Glu	Val	Phe	His	Tyr	Gly	Ser	Leu	Arg	Gly	Arg	Ser	Arg	Arg		35	40	45
Pro	Val	Asn	Leu	Lys	Lys	Trp	Ser	Ile	Thr	Asp	Gly	Tyr	Val	Pro		50	55	60
Ile	Leu	Gly	Asn	Lys	Thr	Leu	Pro	Ser	Arg	Cys	His	Gln	Cys	Val		65	70	75
Ile	Val	Ser	Ser	Ser	Ser	His	Leu	Leu	Gly	Thr	Lys	Leu	Gly	Pro		80	85	90
Glu	Ile	Glu	Arg	Ala	Glu	Cys	Thr	Ile	Arg	Met	Asn	Asp	Ala	Pro		95	100	105
Thr	Thr	Gly	Tyr	Ser	Ala	Asp	Val	Gly	Asn	Lys	Thr	Thr	Tyr	Arg		110	115	120
Val	Val	Ala	His	Ser	Ser	Val	Phe	Arg	Val	Leu	Arg	Arg	Pro	Gln		125	130	135
Glu	Phe	Val	Asn	Arg	Thr	Pro	Glu	Thr	Val	Phe	Ile	Phe	Trp	Gly		140	145	150
Pro	Pro	Ser	Lys	Met	Gln	Lys	Pro	Gln	Gly	Ser	Leu	Val	Arg	Val		155	160	165
Ile	Gln	Arg	Ala	Gly	Leu	Val	Phe	Pro	Asn	Met	Glu	Ala	Tyr	Ala		170	175	180
Val	Ser	Pro	Gly	Arg	Met	Arg	Gln	Phe	Asp	Asp	Leu	Phe	Arg	Gly		185	190	195
Glu	Thr	Gly	Lys	Asp	Arg	Glu	Lys	Ser	His	Ser	Trp	Leu	Ser	Thr		200	205	210
Gly	Trp	Phe	Thr	Met	Val	Ile	Ala	Val	Glu	Leu	Cys	Asp	His	Val		215	220	225
His	Val	Tyr	Gly	Met	Val	Pro	Pro	Asn	Tyr	Cys	Ser	Gln	Arg	Pro		230	235	240
Arg	Leu	Gln	Arg	Met	Pro	Tyr	His	Tyr	Tyr	Glu	Pro	Lys	Gly	Pro		245	250	255
Asp	Glu	Cys	Val	Thr	Tyr	Ile	Gln	Asn	Glu	His	Ser	Arg	Lys	Gly		260	265	270
Asn	His	His	Arg	Phe	Ile	Thr	Glu	Lys	Arg	Val	Phe	Ser	Ser	Trp		275	280	285
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<210> 57

<211> 4277

<212> DNA

<213> Homo sapiens

<400> 57

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<212> PRT

<213> Homo sapiens

<400> 58

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				20					25					30	
Asp	Leu	Asn	Glu	Val	Pro	Gln	Val	Thr	Val	Gln	Pro	Ala	Ser	Thr	
				35					40					45	
Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu	
				50					55					60	
Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu	
				65					70					75	
Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr	
				80					85					90	
Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln	
				95					100					105	
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala	
				110					115					120	
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln	
				125					130					135	
His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys	
				140					145					150	
His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val	
				155					160					165	
Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met	
				170					175					180	
Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu	
				185					190					195	
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val	
				200					205					210	
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr	
				215					220					225	
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile	
				230					235					240	
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser	
				245					250					255	
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser	
				260					265					270	

Val Thr Gly Tyr Asn Lys Thr Arg Phe Leu Leu Ser Asn Leu Leu	275	280	285
Ile Asp Thr Thr Ser Glu Glu Asp Ser Gly Thr Tyr Arg Cys Met	290	295	300
Ala Asp Asn Gly Val Gly Gln Pro Gly Ala Ala Val Ile Leu Tyr	305	310	315
Asn Val Gln Val Phe Glu Pro Pro Glu Val Thr Met Glu Leu Ser	320	325	330
Gln Leu Val Ile Pro Trp Gly Gln Ser Ala Lys Leu Thr Cys Glu	335	340	345
Val Arg Gly Asn Pro Pro Pro Ser Val Leu Trp Leu Arg Asn Ala	350	355	360
Val Pro Leu Ile Ser Ser Gln Arg Leu Arg Leu Ser Arg Arg Ala	365	370	375
Leu Arg Val Leu Ser Met Gly Pro Glu Asp Glu Gly Val Tyr Gln	380	385	390
Cys Met Ala Glu Asn Glu Val Gly Ser Ala His Ala Val Val Gln	395	400	405
Leu Arg Thr Ser Arg Pro Ser Ile Thr Pro Arg Leu Trp Gln Asp	410	415	420
Ala Glu Leu Ala Thr Gly Thr Pro Pro Val Ser Pro Ser Lys Leu	425	430	435
Gly Asn Pro Glu Gln Met Leu Arg Gly Gln Pro Ala Leu Pro Arg	440	445	450
Pro Pro Thr Ser Val Gly Pro Ala Ser Pro Lys Cys Pro Gly Glu	455	460	465
Lys Gly Gln Gly Ala Pro Ala Glu Ala Pro Ile Ile Leu Ser Ser	470	475	480
Pro Arg Thr Ser Lys Thr Asp Ser Tyr Glu Leu Val Trp Arg Pro	485	490	495
Arg His Glu Gly Ser Gly Arg Ala Pro Ile Leu Tyr Tyr Val Val	500	505	510
Lys His Arg Lys Gln Val Thr Asn Ser Ser Asp Asp Trp Thr Ile	515	520	525
Ser Gly Ile Pro Ala Asn Gln His Arg Leu Thr Leu Thr Arg Leu	530	535	540
Asp Pro Gly Ser Leu Tyr Glu Val Glu Met Ala Ala Tyr Asn Cys	545	550	555
Ala Gly Glu Gly Gln Thr Ala Met Val Thr Phe Arg Thr Gly Arg			

	560		565		570
Arg Pro Lys Pro	Glu Ile Met Ala Ser	Lys Glu Gln Gln Ile Gln			
	575	580			585
Arg Asp Asp Pro	Gly Ala Ser Pro Gln	Ser Ser Ser Gln Pro Asp			
	590	595			600
His Gly Arg Leu	Ser Pro Pro Glu Ala	Pro Asp Arg Pro Thr Ile			
	605	610			615
Ser Thr Ala Ser	Glu Thr Ser Val Tyr	Val Thr Trp Ile Pro Arg			
	620	625			630
Gly Asn Gly Gly	Phe Pro Ile Gln Ser	Phe Arg Val Glu Tyr Lys			
	635	640			645
Lys Leu Lys Lys	Val Gly Asp Trp Ile	Leu Ala Thr Ser Ala Ile			
	650	655			660
Pro Pro Ser Arg	Leu Ser Val Glu Ile	Thr Gly Leu Glu Lys Gly			
	665	670			675
Thr Ser Tyr Lys	Phe Arg Val Arg Ala	Leu Asn Met Leu Gly Glu			
	680	685			690
Ser Glu Pro Ser	Ala Pro Ser Arg Pro	Tyr Val Val Ser Gly Tyr			
	695	700			705
Ser Gly Arg Val	Tyr Glu Arg Pro Val	Ala Gly Pro Tyr Ile Thr			
	710	715			720
Phe Thr Asp Ala	Val Asn Glu Thr Thr	Ile Met Leu Lys Trp Met			
	725	730			735
Tyr Ile Pro Ala	Ser Asn Asn Asn Thr	Pro Ile His Gly Phe Tyr			
	740	745			750
Ile Tyr Tyr Arg	Pro Thr Asp Ser Asp	Asn Asp Ser Asp Tyr Lys			
	755	760			765
Lys Asp Met Val	Glu Gly Asp Lys Tyr	Trp His Ser Ile Ser His			
	770	775			780
Leu Gln Pro Glu	Thr Ser Tyr Asp Ile	Lys Met Gln Cys Phe Asn			
	785	790			795
Glu Gly Gly Glu	Ser Glu Phe Ser Asn	Val Met Ile Cys Glu Thr			
	800	805			810
Lys Ala Arg Lys	Ser Ser Gly Gln Pro	Gly Arg Leu Pro Pro Pro			
	815	820			825
Thr Leu Ala Pro	Pro Gln Pro Pro Leu	Pro Glu Thr Ile Glu Arg			
	830	835			840
Pro Val Gly Thr	Gly Ala Met Val Ala	Arg Ser Ser Asp Leu Pro			
	845	850			855

Tyr	Leu	Ile	Val	Gly	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile	
				860					865					870	
Val	Thr	Phe	Ile	Pro	Phe	Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln	
				875					880					885	
Lys	His	Thr	Thr	Asp	Leu	Gly	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro	
				890					895					900	
Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	Leu	Gly	Gly	Leu	Pro	Gly	His	
				905					910					915	
Gln	Ala	Ser	Gly	Gln	Pro	Tyr	Leu	Ser	Gly	Ile	Ser	Gly	Arg	Ala	
				920					925					930	
Cys	Ala	Asn	Gly	Ile	His	Met	Asn	Arg	Gly	Cys	Pro	Ser	Ala	Ala	
				935					940					945	
Val	Gly	Tyr	Pro	Gly	Met	Lys	Pro	Gln	Gln	His	Cys	Pro	Gly	Glu	
				950					955					960	
Leu	Gln	Gln	Gln	Ser	Asp	Thr	Ser	Ser	Leu	Leu	Arg	Gln	Thr	His	
				965					970					975	
Leu	Gly	Asn	Gly	Tyr	Asp	Pro	Gln	Ser	His	Gln	Ile	Thr	Arg	Gly	
				980					985					990	
Pro	Lys	Ser	Ser	Pro	Asp	Glu	Gly	Ser	Phe	Leu	Tyr	Thr	Leu	Pro	
				995					1000					1005	
Asp	Asp	Ser	Thr	His	Gln	Leu	Leu	Gln	Pro	His	His	Asp	Cys	Cys	
				1010					1015					1020	
Gln	Arg	Gln	Glu	Gln	Pro	Ala	Ala	Val	Gly	Gln	Ser	Gly	Val	Arg	
				1025					1030					1035	
Arg	Ala	Pro	Asp	Ser	Pro	Val	Leu	Glu	Ala	Val	Trp	Asp	Pro	Pro	
				1040					1045					1050	
Phe	His	Ser	Gly	Pro	Pro	Cys	Cys	Leu	Gly	Leu	Val	Pro	Val	Glu	
				1055					1060					1065	
Glu	Val	Asp	Ser	Pro	Asp	Ser	Cys	Gln	Val	Ser	Gly	Gly	Asp	Trp	
				1070					1075					1080	
Cys	Pro	Gln	His	Pro	Val	Gly	Ala	Tyr	Val	Gly	Gln	Glu	Pro	Gly	
				1085					1090					1095	
Met	Gln	Leu	Ser	Pro	Gly	Pro	Leu	Val	Arg	Val	Ser	Phe	Glu	Thr	
				1100					1105					1110	
Pro	Pro	Leu	Thr	Ile											
				1115											

<210> 59
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 59
 gggaaacaca gcagtcattg cctgc 25

<210> 60
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 60
 gcacacgtag cctgtcgtg gagc 24

<210> 61
 <211> 42
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-42
 <223> Synthetic construct.

<400> 61
 caccacaaag cccaggtccg gtacagcgtc aaacaagagt gg 42

<210> 62
 <211> 1661
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 678
 <223> unknown base

<400> 62
 cgggaggctg ggtcgtcatg atccggaccc cattgtcggc ctctgcccatt 50
 cgcctgctcc tcccaggctc ccgoggccga ccccgcgca acatgcagcc 100
 cacggggcgc gaggggtccc gcgcgctcag ccggcggtat ctgcggcgtc 150
 tgctgctcct gctactgtg ctgctgtgc ggcagcccgt aaccgcgcg 200
 gagaccacgc cgggcgcccc cagagccctc tccacgctgg gctccccag 250
 cctcttcacc acgccgggtg tccccagcgc cctcactacc ccaggcctca 300
 ctacgccagg caccacaaa accctggacc ttcgggggtcg cgcgcaggcc 350

ctgatgcgga gtttccact cgtggacggc cacaatgacc tgccccaggt 400
cctgagacag cgttacaaga atgtgcttca ggatgttaac ctgcgaaatt 450
tcagccatgg tcagaccagc ctggacaggc ttagagacgg cctcgtgggt 500
gccagttct ggtcagcctc cgtctcatgc cagtcccagg accagactgc 550
cgtgcgcctc gccctggagc agattgacct cattcaccgc atgtgtgcct 600
cctactctga actcgagctt gtgacctcag ctgaaggtct gaacagctct 650
caaaagctgg cctgcctcat tggcgtgnag ggtggtcact cactggacag 700
cagcctctct gtgctgcgca gtttctatgt gctgggggtg cgctacctga 750
cacttacctt cacctgcagt acaccatggg cagagagttc caccaagttc 800
agacaccaca tgtacaccaa cgtcagcgga ttgacaagct ttggtgagaa 850
agtagtagag gagttgaacc gcctgggcat gatgatagat ttgtcctatg 900
catcggacac cttgataaga agggctcctgg aagtgtctca ggctcctgtg 950
atcttctccc actcagctgc cagagctgtg tgtgacaatt tgttgaatgt 1000
tcccgatgat atcctgcagc ttctgaagaa cgggtggcatc gtgatgggtga 1050
cactgtccat gggggtgctg cagtgcgaacc tgcttgctaa cgtgtccact 1100
gtggcagatc actttgacca catcagggca gtcattggat ctgagttcat 1150
cgggattggg ggaaattatg acgggactgg ccgggttcct caggggctgg 1200
aggatgtgtc cacataccca gtccatgatag aggagttgct gagtcgtasc 1250
tggagcgagg aagagcttca aggtgtcctt cgtggaaacc tgctgcgggt 1300
cttcagacaa gtggaaaagg tgagagagga gagcagggcg cagagccccc 1350
tggaggctga gtttccatat gggcaactga gcacatcctg ccaactccac 1400
ctcgtgcctc agaatggaca ccaggctact catctggagg tgaccaagca 1450
gccaaccaat cgggtcccct ggaggctcctc aaatgcctcc ccataccttg 1500
ttccaggcct tgtggctgct gccaccatcc caaccttcac ccagtggctc 1550
tgctgacaca gtcgggtccc gcagaggtca ctgtggcaaa gcctcacaaa 1600
gccccctctc ctagttcatt cacaagcata tgctgagaat aaacatgtta 1650
cacatggaaa a 1661

<210> 63
<211> 487
<212> PRT
<213> Homo sapiens

<220>
 <221> unsure
 <222> 196, 386
 <223> unknown amino acid

<400> 63

Met	Gln	Pro	Thr	Gly	Arg	Glu	Gly	Ser	Arg	Ala	Leu	Ser	Arg	Arg	
1				5					10					15	
Tyr	Leu	Arg	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg	
				20					25					30	
Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala	
				35					40					45	
Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val	
				50					55					60	
Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	
				65					70					75	
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	
				80					85					90	
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	
				95					100					105	
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	
				110					115					120	
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	
				125					130					135	
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp	
				140					145					150	
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His	
				155					160					165	
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	
				170					175					180	
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	
				185					190					195	
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser	
				200					205					210	
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys	
				215					220					225	
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met	
				230					235					240	
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val	
				245					250					255	
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala	

260	265	270
Ser Asp Thr Leu Ile Arg Arg Val Leu Glu Val Ser Gln Ala Pro		
275	280	285
Val Ile Phe Ser His Ser Ala Ala Arg Ala Val Cys Asp Asn Leu		
290	295	300
Leu Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Asn Gly Gly		
305	310	315
Ile Val Met Val Thr Leu Ser Met Gly Val Leu Gln Cys Asn Leu		
320	325	330
Leu Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Arg		
335	340	345
Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp		
350	355	360
Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr		
365	370	375
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu		
380	385	390
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg		
395	400	405
Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val		
410	415	420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser		
425	430	435
His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val		
440	445	450
Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala		
455	460	465
Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro		
470	475	480
Thr Phe Thr Gln Trp Leu Cys		
485		

<210> 64
 <211> 25
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

 <400> 64

ccttcacctg cagtacacca tgggc 25

<210> 65
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 65
gtcacacaca gctctggcag ctgag 25

<210> 66
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-47
<223> Synthetic construct.

<400> 66
ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67
<211> 1564
<212> DNA
<213> Homo sapiens

<400> 67
tgctaggctc tgtcccacaa tgcacccgag agcaggagct gaaagcctct 50
aacaccacaca gatccctcta tgactgcaat gtgaggtgtc cggctttgct 100
ggcccagcaa gcctgataag catgaagctc ttatctttgg tggctgtggt 150
cgggtgtttg ctgggtgccc cagctgaagc caacaagagt tctgaagata 200
tccggtgcaa atgcatctgt ccacctata gaaacatcag tgggcacatt 250
tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300
gcccattgcca gtgcctggcc atgacgtgga ggcctactgc ctgctgtgcg 350
agtgcaggta cgaggagcgc agcaccacca ccatcaaggt catcattgtc 400
atctacctgt ccgtggtggg tgccctgttg ctctacatgg ccttcctgat 450
gctggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500
acaatgagga ggagaatgag gatgctcgct ctatggcagc agctgctgca 550
tccctcgggg gaccccgagc aaacacagtc ctggagcgtg tggaaggtgc 600

ccagcagcgg tggaagctgc aggtgcagga gcagcgggaag acagtcttcg 650
atcggcacaa gatgctcagc tagatgggct ggtgtggttg ggtcaaggcc 700
ccaacaccat ggctgccagc ttccaggctg gacaaagcag ggggctactt 750
ctcccttccc tcggttcagc tcttcccttt aaaagcctgt ggcatttttc 800
ctccttctcc ctaactttag aaatgttgta cttggctatt ttgattaggg 850
aagagggatg tggctctctga tctctgttgt cttcttgggt ctttgggggtt 900
gaagggaggg ggaaggcagg ccagaaggga atggagacat tcgaggcggc 950
ctcaggagtg gatgcgatct gtctctcctg gctccactct tgccgccttc 1000
cagctctgag tcttggaat gttgttacc ttggaagata aagctgggtc 1050
ttcaggaact cagtgtctgg gaggaagca tggcccagca ttcagcatgt 1100
gttcctttct gcagtgggtc ttatcaccac ctccctccca gcccggcgc 1150
ctcagcccca gcccagctc cagccctgag gacagctctg atgggagagc 1200
tgggccccct gagccactg ggtcttcagg gtgcactgga agctgggtgtt 1250
cgctgtcccc tgtgcacttc tcgcaactgg gcattggagt cccatgcata 1300
ctctgtctgcc ggtccctca cctgcacttg aggggtctgg gcagtccctc 1350
ctctccccag tgtccacagt cactgagcca gacggctcgg ttggaacatga 1400
gactcgaggc tgagcgtgga tctgaacacc acagccctg tacttgggtt 1450
gcctcttgtc cctgaacttc gttgtaccag tgcattggaga gaaaattttg 1500
tcctcttgtc ttagagttgt gtgtaaatac aggaagccat cattaaattg 1550
ttttatttct ctca 1564

<210> 68
<211> 183
<212> PRT
<213> Homo sapiens

<400> 68
Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val
1 5 10 15
Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys
20 25 30
Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn
35 40 45
Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
50 55 60

Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu
65 70 75

Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val
80 85 90

Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr
95 100 105

Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp
110 115 120

Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala
125 130 135

Arg Ser Met Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala
140 145 150

Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys
155 160 165

Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys
170 175 180

Met Leu Ser

<210> 69
<211> 3170
<212> DNA
<213> Homo sapiens

<400> 69
agcgggtctc gcttggttc cgctaatttc tgtcctgagg cgtgagactg 50
agttcatagg gtcttggttc cccgaaccag gaagggttga gggaacacaa 100
tctgcaagcc cccgcgaccc aagtgagggg ccccggtgtg gggtcctccc 150
tccctttgca ttcccacccc tccgggcttt gcgttttctt ggggaccccc 200
tcgccgggag atggccgcgt tgatgcggag caaggattcg tctgctgcc 250
tgctcctact ggccgcggtg ctgatggtgg agagctcaca gatcggcagt 300
tcgcgggcca aactcaactc catcaagtcc tctctgggag gggagacgcc 350
tggtcaggcc gccaatcgat ctgcgggcat gtaccaagga ctggcattcg 400
gcggcagtaa gaagggcaaa aacctggggc aggcctaccc ttgtagcagt 450
gataaggagt gtgaagttgg gaggtattgc cacagtcccc accaaggatc 500
atcggcctgc atggtgtgtc ggagaaaaaa gaagcgtgc caccgagatg 550
gcatgtgtcg cccagtagc cgctgcaata atggcatctg tatcccagtt 600
actgaaagca tcttaacccc tcacatcccg gctctggatg gtactcggca 650

cagagatcga aaccacggtc attactcaaa ccatgacttg ggatggcaga 700
atctaggaag accacacact aagatgtcac atataaaagg gcatgaagga 750
gaccctgcc tacgatcatc agactgcatt gaagggtttt gctgtgctcg 800
tcatttctgg accaaaatct gcaaaccagt gctccatcag ggggaagtct 850
gtaccaaaaca acgcaagaag ggttctcatg ggctggaaat tttccagcgt 900
tgcgactgtg cgaagggcct gtcttgcaaa gtatggaaag atgccaccta 950
ctcctccaaa gccagactcc atgtgtgtca gaaaatttga tcaccattga 1000
ggaacatcat caattgcaga ctgtgaagtt gtgtatttaa tgcattatag 1050
catggtggaa aataaggttc agatgcagaa gaatggctaa aataagaaac 1100
gtgataagaa tatagatgat cacaaaaagg gagaaagaaa acatgaactg 1150
aatagattag aatgggtgac aaatgcagtg cagccagtgt ttccattatg 1200
caacttgtct atgtaaataa tgtacacatt tgtggaaaat gctattatta 1250
agagaacaag cacacagtgg aaattactga tgagtagcat gtgactttcc 1300
aagagtttag gttgtgctgg aggagaggtt tccttcagat tgctgattgc 1350
ttatacaaat aacctacatg ccagatttct attcaacggt agagtttaac 1400
aaaatactcc tagaataact tgttatacaa taggttctaa aaataaaatt 1450
gctaaacaag aaatgaaaac atggagcatt gttaatttac aacagaaaat 1500
taccttttga tttgtaacac tacttctgct gttcaatcaa gagtcttggt 1550
agataagaaa aaaatcagtc aatatttcca aataattgca aaataatggc 1600
cagttgttta ggaaggcctt taggaagaca aataaataac aaacaaacag 1650
ccacaaatac ttttttttca aaattttagt tttacctgta attaataaga 1700
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<210> 72
<211> 363
<212> PRT
<213> Homo sapiens

<400> 72
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20 25 30
Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser
35 40 45
Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr
50 55 60
Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr
65 70 75
Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val
80 85 90
Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val
95 100 105
Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val
110 115 120
Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys
125 130 135
Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys
140 145 150
Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser
155 160 165
Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg
170 175 180
Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro
185 190 195
Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu
200 205 210
Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro
215 220 225

Ser Ser Glu Asn Ser Asn Gln Ile Pro Ile Ser Leu Tyr Ser Lys
 230 235 240
 Ser Leu Ser Glu Pro Leu Asn Thr Ser Leu Ser Met Thr Ser Ala
 245 250 255
 Val Gln Asn Ser Thr Tyr Thr Thr Ser Val Ile Thr Ser Cys Ser
 260 265 270
 Leu Thr Ser Ser Ser Leu Asn Ser Ala Ser Pro Val Ala Met Ser
 275 280 285
 Ser Ser Tyr Asp Gln Ser Ser Val His Asn Arg Ile Pro Tyr Gln
 290 295 300
 Ser Pro Val Ser Ser Ser Glu Ser Ala Pro Gly Thr Ile Met Asn
 305 310 315
 Gly His Gly Gly Gly Arg Ser Gln Gln Thr Leu Asp Ser Lys Tyr
 320 325 330
 Ser Ser Lys Leu Leu Leu Ser Trp Leu Val Pro Thr Lys Gln Arg
 335 340 345
 Lys Arg Ile Ala His Val Met Trp Lys Thr Pro Val Gly Gln Trp
 350 355 360
 Leu Ile Arg

<210> 73
 <211> 26
 <212> DNA
 <213> Artificial
 <220>
 <221> Artificial sequence
 <222> 1-26
 <223> Synthetic construct.
 <400> 73
 aattcatggc aaatatttcc ottccc 26

<210> 74
 <211> 22
 <212> DNA
 <213> Artificial
 <220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.
 <400> 74
 tggtaaactg gcccaaactc gg 22
 <210> 75
 <211> 50

<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-50
<223> Synthetic construct

<400> 75
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<210> 76
<211> 1989
<212> DNA
<213> Homo sapiens

<400> 76
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 ccactctcag caccacacat ttgcattctg tgggtggacct gccaccatca 1950
 caataaagtc cccatctgat ttttaaaaaa aaaaaaaaaa 1989

<210> 77

<211> 341

<212> PRT

<213> Homo sapiens

<400> 77

Met	Ala	Leu	Pro	Ser	Arg	Ile	Leu	Leu	Trp	Lys	Leu	Val	Leu	Leu
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Gln	Ser	Ser	Ala	Val	Leu	Leu	His	Ser	Ala	Val	Glu	Glu	Thr	Asp
				20					25					30
Ala	Gly	Leu	Tyr	Thr	Cys	Asn	Leu	His	His	His	Tyr	Cys	His	Leu
				35					40					45
Tyr	Glu	Ser	Leu	Ala	Val	Arg	Leu	Glu	Val	Thr	Asp	Gly	Pro	Pro
				50					55					60
Ala	Thr	Pro	Ala	Tyr	Trp	Asp	Gly	Glu	Lys	Glu	Val	Leu	Ala	Val
				65					70					75

Ala	Arg	Gly	Ala	Pro	Ala	Leu	Leu	Thr	Cys	Val	Asn	Arg	Gly	His	80	85	90
Val	Trp	Thr	Asp	Arg	His	Val	Glu	Glu	Ala	Gln	Gln	Val	Val	His	95	100	105
Trp	Asp	Arg	Gln	Pro	Pro	Gly	Val	Pro	His	Asp	Arg	Ala	Asp	Arg	110	115	120
Leu	Leu	Asp	Leu	Tyr	Ala	Ser	Gly	Glu	Arg	Arg	Ala	Tyr	Gly	Pro	125	130	135
Leu	Phe	Leu	Arg	Asp	Arg	Val	Ala	Val	Gly	Ala	Asp	Ala	Phe	Glu	140	145	150
Arg	Gly	Asp	Phe	Ser	Leu	Arg	Ile	Glu	Pro	Leu	Glu	Val	Ala	Asp	155	160	165
Glu	Gly	Thr	Tyr	Ser	Cys	His	Leu	His	His	His	Tyr	Cys	Gly	Leu	170	175	180
His	Glu	Arg	Arg	Val	Phe	His	Leu	Thr	Val	Ala	Glu	Pro	His	Ala	185	190	195
Glu	Pro	Pro	Pro	Arg	Gly	Ser	Pro	Gly	Asn	Gly	Ser	Ser	His	Ser	200	205	210
Gly	Ala	Pro	Gly	Pro	Asp	Pro	Thr	Leu	Ala	Arg	Gly	His	Asn	Val	215	220	225
Ile	Asn	Val	Ile	Val	Pro	Glu	Ser	Arg	Ala	His	Phe	Phe	Gln	Gln	230	235	240
Leu	Gly	Tyr	Val	Leu	Ala	Thr	Leu	Leu	Leu	Phe	Ile	Leu	Leu	Leu	245	250	255
Val	Thr	Val	Leu	Leu	Ala	Ala	Arg	Arg	Arg	Arg	Gly	Gly	Tyr	Glu	260	265	270
Tyr	Ser	Asp	Gln	Lys	Ser	Gly	Lys	Ser	Lys	Gly	Lys	Asp	Val	Asn	275	280	285
Leu	Ala	Glu	Phe	Ala	Val	Ala	Ala	Gly	Asp	Gln	Met	Leu	Tyr	Arg	290	295	300
Ser	Glu	Asp	Ile	Gln	Leu	Asp	Tyr	Lys	Asn	Asn	Ile	Leu	Lys	Glu	305	310	315
Arg	Ala	Glu	Leu	Ala	His	Ser	Pro	Leu	Pro	Ala	Lys	Tyr	Ile	Asp	320	325	330
Leu	Asp	Lys	Gly	Phe	Arg	Lys	Glu	Asn	Cys	Lys					335	340	

<210> 78
 <211> 2243
 <212> DNA
 <213> Homo sapiens

<400> 78

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<210> 79

<211> 475

<212> PRT

<213> Homo sapiens

<400> 79

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Thr	Tyr	Gly	Thr	Thr	Ser	Ser	Ser	Leu	Arg	Ala	Asp	Gln	Glu	Ala
			20						25					30

Leu	Leu	Glu	Lys	Leu	Leu	Asp	Arg	Pro	Pro	Pro	Gly	Leu	Gln	Arg
			35						40					45

Pro	Glu	Asp	Arg	Phe	Cys	Gly	Thr	Tyr	Ile	Ile	Phe	Phe	Ser	Leu
			50						55					60

Gly	Ile	Gly	Ser	Leu	Leu	Pro	Trp	Asn	Phe	Phe	Ile	Thr	Ala	Lys
			65						70					75

Glu	Tyr	Trp	Met	Phe	Lys	Leu	Arg	Asn	Ser	Ser	Ser	Pro	Ala	Thr
			80						85					90

Gly	Glu	Asp	Pro	Glu	Gly	Ser	Asp	Ile	Leu	Asn	Tyr	Phe	Glu	Ser
			95						100					105

Tyr	Leu	Ala	Val	Ala	Ser	Thr	Val	Pro	Ser	Met	Leu	Cys	Leu	Val	110	115	120
Ala	Asn	Phe	Leu	Leu	Val	Asn	Arg	Val	Ala	Val	His	Ile	Arg	Val	125	130	135
Leu	Ala	Ser	Leu	Thr	Val	Ile	Leu	Ala	Ile	Phe	Met	Val	Ile	Thr	140	145	150
Ala	Leu	Val	Lys	Val	Asp	Thr	Ser	Ser	Trp	Thr	Arg	Gly	Phe	Phe	155	160	165
Ala	Val	Thr	Ile	Val	Cys	Met	Val	Ile	Leu	Ser	Gly	Ala	Ser	Thr	170	175	180
Val	Phe	Ser	Ser	Ser	Ile	Tyr	Gly	Met	Thr	Gly	Ser	Phe	Pro	Met	185	190	195
Arg	Asn	Ser	Gln	Ala	Leu	Ile	Ser	Gly	Gly	Ala	Met	Gly	Gly	Thr	200	205	210
Val	Ser	Ala	Val	Ala	Ser	Leu	Val	Asp	Leu	Ala	Ala	Ser	Ser	Asp	215	220	225
Val	Arg	Asn	Ser	Ala	Leu	Ala	Phe	Phe	Leu	Thr	Ala	Thr	Ile	Phe	230	235	240
Leu	Val	Leu	Cys	Met	Gly	Leu	Tyr	Leu	Leu	Leu	Ser	Arg	Leu	Glu	245	250	255
Tyr	Ala	Arg	Tyr	Tyr	Met	Arg	Pro	Val	Leu	Ala	Ala	His	Val	Phe	260	265	270
Ser	Gly	Glu	Glu	Glu	Leu	Pro	Gln	Asp	Ser	Leu	Ser	Ala	Pro	Ser	275	280	285
Val	Ala	Ser	Arg	Phe	Ile	Asp	Ser	His	Thr	Pro	Pro	Leu	Arg	Pro	290	295	300
Ile	Leu	Lys	Lys	Thr	Ala	Ser	Leu	Gly	Phe	Cys	Val	Thr	Tyr	Val	305	310	315
Phe	Phe	Ile	Thr	Ser	Leu	Ile	Tyr	Pro	Ala	Val	Cys	Thr	Asn	Ile	320	325	330
Glu	Ser	Leu	Asn	Lys	Gly	Ser	Gly	Ser	Leu	Trp	Thr	Thr	Lys	Phe	335	340	345
Phe	Ile	Pro	Leu	Thr	Thr	Phe	Leu	Leu	Tyr	Asn	Phe	Ala	Asp	Leu	350	355	360
Cys	Gly	Arg	Gln	Leu	Thr	Ala	Trp	Ile	Gln	Val	Pro	Gly	Pro	Asn	365	370	375
Ser	Lys	Ala	Leu	Pro	Gly	Phe	Val	Leu	Leu	Arg	Thr	Cys	Leu	Ile	380	385	390
Pro	Leu	Phe	Val	Leu	Cys	Asn	Tyr	Gln	Pro	Arg	Val	His	Leu	Lys			

	395		400		405
Thr Val Val Phe	Gln Ser Asp Val Tyr	Pro Ala Leu Leu Ser	Ser		
	410	415	420		
Leu Leu Gly Leu	Ser Asn Gly Tyr Leu	Ser Thr Leu Ala Leu	Leu		
	425	430	435		
Tyr Gly Pro Lys	Ile Val Pro Arg Glu	Leu Ala Glu Ala Thr	Gly		
	440	445	450		
Val Val Met Ser	Phe Tyr Val Cys Leu	Gly Leu Thr Leu Gly	Ser		
	455	460	465		
Ala Cys Ser Thr	Leu Leu Val His Leu	Ile			
	470	475			

<210> 80
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 80
 ttttgcggtc accattgtct gc 22

<210> 81
 <211> 23
 <212> DNA
 <213> Homo sapiens

<220>
 <221> Artificial sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 81
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<210> 82
 <211> 49
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-49
 <223> Synthetic construct.

<400> 82
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<210> 83
 <211> 1844

<212> DNA

<213> Homo sapiens

<400> 83

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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84

<211> 567

<212> PRT

<213> Homo sapiens

<400> 84

Met	Ala	Pro	Leu	Ala	Leu	His	Leu	Leu	Val	Leu	Val	Pro	Ile	Leu	1	5	10	15
Leu	Ser	Leu	Val	Ala	Ser	Gln	Asp	Trp	Lys	Ala	Glu	Arg	Ser	Gln	20	25	30	
Asp	Pro	Phe	Glu	Lys	Cys	Met	Gln	Asp	Pro	Asp	Tyr	Glu	Gln	Leu	35	40	45	
Leu	Lys	Val	Val	Thr	Trp	Gly	Leu	Asn	Arg	Thr	Leu	Lys	Pro	Gln	50	55	60	
Arg	Val	Ile	Val	Val	Gly	Ala	Gly	Val	Ala	Gly	Leu	Val	Ala	Ala	65	70	75	
Lys	Val	Leu	Ser	Asp	Ala	Gly	His	Lys	Val	Thr	Ile	Leu	Glu	Ala	80	85	90	
Asp	Asn	Arg	Ile	Gly	Gly	Arg	Ile	Phe	Thr	Tyr	Arg	Asp	Gln	Asn	95	100	105	
Thr	Gly	Trp	Ile	Gly	Glu	Leu	Gly	Ala	Met	Arg	Met	Pro	Ser	Ser	110	115	120	
His	Arg	Ile	Leu	His	Lys	Leu	Cys	Gln	Gly	Leu	Gly	Leu	Asn	Leu	125	130	135	
Thr	Lys	Phe	Thr	Gln	Tyr	Asp	Lys	Asn	Thr	Trp	Thr	Glu	Val	His	140	145	150	
Glu	Val	Lys	Leu	Arg	Asn	Tyr	Val	Val	Glu	Lys	Val	Pro	Glu	Lys	155	160	165	

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Gly	Ser	Pro	His	Ser	Leu	Glu	Ala	Leu	Arg	Asp	Ala	Ala	Pro	Ser	
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Gln	Gly	Leu	Asn	Phe	Leu	Leu	Leu	Phe	Thr	Lys	Met	Leu	Phe	Ile	
				50					55					60	
Phe	Asn	Phe	Leu	Phe	Ser	Pro	Leu	Pro	Thr	Pro	Ala	Leu	Ile	Cys	
				65					70					75	
Ile	Leu	Thr	Phe	Gly	Ala	Ala	Ile	Phe	Leu	Trp	Leu	Ile	Thr	Arg	
				80					85					90	
Pro	Gln	Pro	Val	Leu	Pro	Leu	Leu	Asp	Leu	Asn	Asn	Gln	Ser	Val	
				95					100					105	
Gly	Ile	Glu	Gly	Gly	Ala	Arg	Lys	Gly	Val	Ser	Gln	Lys	Asn	Asn	
				110					115					120	
Asp	Leu	Thr	Ser	Cys	Cys	Phe	Ser	Asp	Ala	Lys	Thr	Met	Tyr	Glu	
				125					130					135	
Val	Phe	Gln	Arg	Gly	Leu	Ala	Val	Ser	Asp	Asn	Gly	Pro	Cys	Leu	
				140					145					150	
Gly	Tyr	Arg	Lys	Pro	Asn	Gln	Pro	Tyr	Arg	Trp	Leu	Ser	Tyr	Lys	
				155					160					165	
Gln	Val	Ser	Asp	Arg	Ala	Glu	Tyr	Leu	Gly	Ser	Cys	Leu	Leu	His	
				170					175					180	
Lys	Gly	Tyr	Lys	Ser	Ser	Pro	Asp	Gln	Phe	Val	Gly	Ile	Phe	Ala	
				185					190					195	
Gln	Asn	Arg	Pro	Glu	Trp	Ile	Ile	Ser	Glu	Leu	Ala	Cys	Tyr	Thr	
				200					205					210	
Tyr	Ser	Met	Val	Ala	Val	Pro	Leu	Tyr	Asp	Thr	Leu	Gly	Pro	Glu	
				215					220					225	
Ala	Ile	Val	His	Ile	Val	Asn	Lys	Ala	Asp	Ile	Ala	Met	Val	Ile	
				230					235					240	
Cys	Asp	Thr	Pro	Gln	Lys	Ala	Leu	Val	Leu	Ile	Gly	Asn	Val	Glu	
				245					250					255	
Lys	Gly	Phe	Thr	Pro	Ser	Leu	Lys	Val	Ile	Ile	Leu	Met	Asp	Pro	
				260					265					270	
Phe	Asp	Asp	Asp	Leu	Lys	Gln	Arg	Gly	Glu	Lys	Ser	Gly	Ile	Glu	
				275					280					285	
Ile	Leu	Ser	Leu	Tyr	Asp	Ala	Glu	Asn	Leu	Gly	Lys	Glu	His	Phe	
				290					295					300	
Arg	Lys	Pro	Val	Pro	Pro	Ser	Pro	Glu	Asp	Leu	Ser	Val	Ile	Cys	
				305					310					315	
Phe	Thr	Ser	Gly	Thr	Thr	Gly	Asp	Pro	Lys	Gly	Ala	Met	Ile	Thr	

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His Gln Asn Ile Val Ser Asn Ala Ala	Ala Phe Leu Lys Cys Val	
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Glu His Ala Tyr Glu Pro Thr Pro Asp	Asp Val Ala Ile Ser Tyr	
350	355	360
Leu Pro Leu Ala His Met Phe Glu Arg	Ile Val Gln Ala Val Val	
365	370	375
Tyr Ser Cys Gly Ala Arg Val Gly Phe	Phe Gln Gly Asp Ile Arg	
380	385	390
Leu Leu Ala Asp Asp Met Lys Thr Leu	Lys Pro Thr Leu Phe Pro	
395	400	405
Ala Val Pro Arg Leu Leu Asn Arg Ile	Tyr Asp Lys Val Gln Asn	
410	415	420
Glu Ala Lys Thr Pro Leu Lys Lys Phe	Leu Leu Lys Leu Ala Val	
425	430	435
Ser Ser Lys Phe Lys Glu Leu Gln Lys	Gly Ile Ile Arg His Asp	
440	445	450
Ser Phe Trp Asp Lys Leu Ile Phe Ala	Lys Ile Gln Asp Ser Leu	
455	460	465
Gly Gly Arg Val Arg Val Ile Val Thr	Gly Ala Ala Pro Met Ser	
470	475	480
Thr Ser Val Met Thr Phe Phe Arg Ala	Ala Met Gly Cys Gln Val	
485	490	495
Tyr Glu Ala Tyr Gly Gln Thr Glu Cys	Thr Gly Gly Cys Thr Phe	
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Thr Leu Pro Gly Asp Trp Thr Ser Gly	His Val Gly Val Pro Leu	
515	520	525
Ala Cys Asn Tyr Val Lys Leu Glu Asp	Val Ala Asp Met Asn Tyr	
530	535	540
Phe Thr Val Asn Asn Glu Gly Glu Val	Cys Ile Lys Gly Thr Asn	
545	550	555
Val Phe Lys Gly Tyr Leu Lys Asp Pro	Glu Lys Thr Gln Glu Ala	
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Leu Asp Ser Asp Gly Trp Leu His Thr	Gly Asp Ile Gly Arg Trp	
575	580	585
Leu Pro Asn Gly Thr Leu Lys Ile Ile	Asp Arg Lys Lys Asn Ile	
590	595	600
Phe Lys Leu Ala Gln Gly Glu Tyr Ile	Ala Pro Glu Lys Ile Glu	
605	610	615

Asn	Ile	Tyr	Asn	Arg	Ser	Gln	Pro	Val	Leu	Gln	Ile	Phe	Val	His
				620					625					630
Gly	Glu	Ser	Leu	Arg	Ser	Ser	Leu	Val	Gly	Val	Val	Val	Pro	Asp
				635					640					645
Thr	Asp	Val	Leu	Pro	Ser	Phe	Ala	Ala	Lys	Leu	Gly	Val	Lys	Gly
				650					655					660
Ser	Phe	Glu	Glu	Leu	Cys	Gln	Asn	Gln	Val	Val	Arg	Glu	Ala	Ile
				665					670					675
Leu	Glu	Asp	Leu	Gln	Lys	Ile	Gly	Lys	Glu	Ser	Gly	Leu	Lys	Thr
				680					685					690
Phe	Glu	Gln	Val	Lys	Ala	Ile	Phe	Leu	His	Pro	Glu	Pro	Phe	Ser
				695					700					705
Ile	Glu	Asn	Gly	Leu	Leu	Thr	Pro	Thr	Leu	Lys	Ala	Lys	Arg	Gly
				710					715					720
Glu	Leu	Ser	Lys	Tyr	Phe	Arg	Thr	Gln	Ile	Asp	Ser	Leu	Tyr	Glu
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His Ile Gln Asp

<210> 87
 <211> 2725
 <212> DNA
 <213> Homo sapiens

<400> 87
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<210> 88

<211> 660

<212> PRT

<213> Homo sapiens

<400> 88

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				20					25					30
Asn	Gln	Arg	Ala	Leu	Arg	Arg	Phe	Cys	Gln	Thr	Gly	Ala	Val	Leu
				35					40					45
Phe	Leu	Leu	Val	Thr	Val	Ile	Val	Asn	Ile	Lys	Leu	Ile	Leu	Asp
				50					55					60
Thr	Arg	Arg	Ala	Ile	Ser	Glu	Ala	Asn	Glu	Asp	Pro	Glu	Pro	Glu
				65					70					75
Gln	Asp	Tyr	Asp	Glu	Ala	Leu	Gly	Arg	Leu	Glu	Pro	Pro	Arg	Arg
				80					85					90
Arg	Gly	Ser	Gly	Pro	Arg	Arg	Val	Leu	Asp	Val	Glu	Val	Tyr	Ser
				95					100					105
Ser	Arg	Ser	Lys	Val	Tyr	Val	Ala	Val	Asp	Gly	Thr	Thr	Val	Leu
				110					115					120
Glu	Asp	Glu	Ala	Arg	Glu	Gln	Gly	Arg	Gly	Ile	His	Val	Ile	Val
				125					130					135

425	430	435
Asp Pro Ala Leu Leu Tyr Arg Val Glu	Thr Met Pro Gly Leu Gly	
440	445	450
Trp Val Leu Arg Arg Ser Leu Tyr Lys	Glu Glu Leu Glu Pro Lys	
455	460	465
Trp Pro Thr Pro Glu Lys Leu Trp Asp	Trp Asp Met Trp Met Arg	
470	475	480
Met Pro Glu Gln Arg Arg Gly Arg Glu	Cys Ile Ile Pro Asp Val	
485	490	495
Ser Arg Ser Tyr His Phe Gly Ile Val	Gly Leu Asn Met Asn Gly	
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Tyr Phe His Glu Ala Tyr Phe Lys Lys	His Lys Phe Asn Thr Val	
515	520	525
Pro Gly Val Gln Leu Arg Asn Val Asp	Ser Leu Lys Lys Glu Ala	
530	535	540
Tyr Glu Val Glu Val His Arg Leu Leu	Ser Glu Ala Glu Val Leu	
545	550	555
Asp His Ser Lys Asn Pro Cys Glu Asp	Ser Phe Leu Pro Asp Thr	
560	565	570
Glu Gly His Thr Tyr Val Ala Phe Ile	Arg Met Glu Lys Asp Asp	
575	580	585
Asp Phe Thr Thr Trp Thr Gln Leu Ala	Lys Cys Leu His Ile Trp	
590	595	600
Asp Leu Asp Val Arg Gly Asn His Arg	Gly Leu Trp Arg Leu Phe	
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Arg Lys Lys Asn His Phe Leu Val Val	Gly Val Pro Ala Ser Pro	
620	625	630
Tyr Ser Val Lys Lys Pro Pro Ser Val	Thr Pro Ile Phe Leu Glu	
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Pro Pro Pro Lys Glu Glu Gly Ala Pro	Gly Ala Pro Glu Gln Thr	
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<210> 89

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 89

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<210> 90
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 90
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<210> 91
 <211> 24
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-24
 <223> Synthetic construct.

<400> 91
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<210> 92
 <211> 26
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-26
 <223> Synthetic construct.

<400> 92
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<210> 93
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 <212> DNA
 <213> Artificial

<220>
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 <223> Synthetic construct.

<400> 93
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<210> 94
 <211> 3037
 <212> DNA
 <213> Homo sapiens

THE

<400> 94
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<212> PRT
<213> Homo sapiens

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35 40 45
Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His
50 55 60
Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser
65 70 75
Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser
80 85 90
Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His
95 100 105
Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu
110 115 120
Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp
125 130 135
Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu
140 145 150
Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala
155 160 165
Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val
170 175 180
Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser
185 190 195
Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His
200 205 210
Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr
215 220 225
Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val

	230		235		240									
Asn	Ala	Thr	Gly	Val	Ala	Met	Leu	Phe	Ser	Ala	Gly	Thr	Phe	Leu
				245					250					255
Tyr	Val	Ala	Thr	Val	His	Val	Leu	Pro	Glu	Val	Gly	Gly	Ile	Gly
				260					265					270
His	Ser	His	Lys	Pro	Asp	Ala	Thr	Gly	Gly	Arg	Gly	Leu	Ser	Arg
				275					280					285
Leu	Glu	Val	Ala	Ala	Leu	Val	Leu	Gly	Cys	Leu	Ile	Pro	Leu	Ile
				290					295					300
Leu	Ser	Val	Gly	His	Gln	His								
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 <213> Artificial

<220>
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 <222> 1-25
 <223> Synthetic construct.

<400> 96
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<210> 97
 <211> 25
 <212> DNA
 <213> Artificial

<220>
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 <223> Synthetic construct.

<400> 97
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 <211> 50
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-50
 <223> Synthetic construct.

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<210> 99
 <211> 1429

<212> DNA

<213> Homo sapiens

<400> 99

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ctgattttga gatgatgggc ttgggaaacg ggcgtcgcag catgaagtcg 150
ccgcccctcg tgctggccgc cctggtggcc tgcacatcg tcttgggctt 200
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gcttgacaaa atccagtcca gccacaactt ccagctggag agcgtcaaca 400
agctgtacca ggacgaaaag gcggttttgg tgaataacat caccacaggt 450
gagaggctca tccgagtgct gcaagaccag ttaaagacct tgcagaggaa 500
ttacggcagg ctgcagcagg atgtcctcca gtttcagaag aaccagacca 550
acctggagag gaagttctcc tacgacctga gccagtgcac caatcagatg 600
aaggaggtga aggaacagtg tgaggagcga atagaagagg tcaccaaaaa 650
ggggaatgaa gctgtagctt ccagagacct gagtgaaaac aacgaccaga 700
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ggaatcatat actctgaatt gaactggaat cacatatattt acaacagggc 1350

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<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

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				20					25					30	
Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg	
				35					40					45	
Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg	
				50					55					60	
Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu	
				65					70					75	
Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe	
				80					85					90	
Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val	
				95					100					105	
Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu	
				110					115					120	
Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln	
				125					130					135	
Gln	Asp	Val	Leu	Gln	Phe	Gln	Lys	Asn	Gln	Thr	Asn	Leu	Glu	Arg	
				140					145					150	
Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile	Asn	Gln	Met	Lys	Glu	
				155					160					165	
Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu	Val	Thr	Lys	Lys	
				170					175					180	
Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp	
				185					190					195	
Gln	Arg	Gln	Gln	Leu	Gln	Ala	Leu	Ser	Glu	Pro	Gln	Pro	Arg	Leu	
				200					205					210	
Gln	Ala	Ala	Gly	Leu	Pro	His	Thr	Glu	Val	Pro	Gln	Gly	Lys	Gly	
				215					220					225	
Asn	Val	Leu	Gly	Asn	Ser	Lys	Ser	Gln	Thr	Pro	Ala	Pro	Ser	Ser	
				230					235					240	

Glu Val Val Leu Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr	245	250	255
Asn Glu Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu	260	265	270
Pro Gln Glu Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val	275	280	285
Gly Gly Arg Gly Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro	290	295	300
Gln Val Gln Ala Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met	305	310	315
Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu	320	325	330
Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu	335	340	345
Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser	350	355	360
Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile	365	370	375
Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu	380	385	390
Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu	395	400	

<210> 101
 <211> 3671
 <212> DNA
 <213> Homo sapiens

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<210> 102

<211> 1089

<212> PRT

<213> Homo sapiens

<400> 102

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				20					25					30	
Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro	
				35					40					45	
Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala	
				50					55					60	
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile	
				65					70					75	
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val	
				80					85					90	
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser	
				95					100					105	
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu	
				110					115					120	
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu	
				125					130					135	
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly	
				140					145					150	
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys	
				155					160					165	
Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp	
				170					175					180	
Thr	Trp	Lys	Asp	Leu	Phe	Pro	Gly	Ala	Phe	Ser	Lys	Ala	Phe	Phe	
				185					190					195	
Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly	

				200					205					210
Ile	Leu	Glu	His	Leu 215	Tyr	Pro	Thr	Met	Asp 220	Ser	Gly	Glu	Trp	Asp 225
Val	Leu	Ile	Ala	His 230	Phe	Leu	Gly	Val	Asp 235	His	Cys	Gly	His	Lys 240
His	Gly	Pro	His	His 245	Pro	Glu	Met	Ala	Lys 250	Lys	Leu	Ser	Gln	Met 255
Asp	Gln	Val	Ile	Gln 260	Gly	Leu	Val	Glu	Arg 265	Leu	Glu	Asn	Asp	Thr 270
Leu	Leu	Val	Val	Ala 275	Gly	Asp	His	Gly	Met 280	Thr	Thr	Asn	Gly	Asp 285
His	Gly	Gly	Asp	Ser 290	Glu	Leu	Glu	Val	Ser 295	Ala	Ala	Leu	Phe	Leu 300
Tyr	Ser	Pro	Thr	Ala 305	Val	Phe	Pro	Ser	Thr 310	Pro	Pro	Glu	Glu	Pro 315
Glu	Val	Ile	Pro	Gln 320	Val	Ser	Leu	Val	Pro 325	Thr	Leu	Ala	Leu	Leu 330
Leu	Gly	Leu	Pro	Ile 335	Pro	Phe	Gly	Asn	Ile 340	Gly	Glu	Val	Met	Ala 345
Glu	Leu	Phe	Ser	Gly 350	Gly	Glu	Asp	Ser	Gln 355	Pro	His	Ser	Ser	Ala 360
Leu	Ala	Gln	Ala	Ser 365	Ala	Leu	His	Leu	Asn 370	Ala	Gln	Gln	Val	Ser 375
Arg	Phe	Leu	His	Thr 380	Tyr	Ser	Ala	Ala	Thr 385	Gln	Asp	Leu	Gln	Ala 390
Lys	Glu	Leu	His	Gln 395	Leu	Gln	Asn	Leu	Phe 400	Ser	Lys	Ala	Ser	Ala 405
Asp	Tyr	Gln	Trp	Leu 410	Leu	Gln	Ser	Pro	Lys 415	Gly	Ala	Glu	Ala	Thr 420
Leu	Pro	Thr	Val	Ile 425	Ala	Glu	Leu	Gln	Gln 430	Phe	Leu	Arg	Gly	Ala 435
Arg	Ala	Met	Cys	Ile 440	Glu	Ser	Trp	Ala	Arg 445	Phe	Ser	Leu	Val	Arg 450
Met	Ala	Gly	Gly	Thr 455	Ala	Leu	Leu	Ala	Ala 460	Ser	Cys	Phe	Ile	Cys 465
Leu	Leu	Ala	Ser	Gln 470	Trp	Ala	Ile	Ser	Pro 475	Gly	Phe	Pro	Phe	Cys 480
Pro	Leu	Leu	Leu	Thr 485	Pro	Val	Ala	Trp	Gly 490	Leu	Val	Gly	Ala	Ile 495

Ala	Tyr	Ala	Gly	Leu 500	Leu	Gly	Thr	Ile	Glu 505	Leu	Lys	Leu	Asp	Leu 510
Val	Leu	Leu	Gly	Ala 515	Val	Ala	Ala	Val	Ser 520	Ser	Phe	Leu	Pro	Phe 525
Leu	Trp	Lys	Ala	Trp 530	Ala	Gly	Trp	Gly	Ser 535	Lys	Arg	Pro	Leu	Ala 540
Thr	Leu	Phe	Pro	Ile 545	Pro	Gly	Pro	Val	Leu 550	Leu	Leu	Leu	Leu	Phe 555
Arg	Leu	Ala	Val	Phe 560	Phe	Ser	Asp	Ser	Phe 565	Val	Val	Ala	Glu	Ala 570
Arg	Ala	Thr	Pro	Phe 575	Leu	Leu	Gly	Ser	Phe 580	Ile	Leu	Leu	Leu	Val 585
Val	Gln	Leu	His	Trp 590	Glu	Gly	Gln	Leu	Leu 595	Pro	Pro	Lys	Leu	Leu 600
Thr	Met	Pro	Arg	Leu 605	Gly	Thr	Ser	Ala	Thr 610	Thr	Asn	Pro	Pro	Arg 615
His	Asn	Gly	Ala	Tyr 620	Ala	Leu	Arg	Leu	Gly 625	Ile	Gly	Leu	Leu	Leu 630
Cys	Thr	Arg	Leu	Ala 635	Gly	Leu	Phe	His	Arg 640	Cys	Pro	Glu	Glu	Thr 645
Pro	Val	Cys	His	Ser 650	Ser	Pro	Trp	Leu	Ser 655	Pro	Leu	Ala	Ser	Met 660
Val	Gly	Gly	Arg	Ala 665	Lys	Asn	Leu	Trp	Tyr 670	Gly	Ala	Cys	Val	Ala 675
Ala	Leu	Val	Ala	Leu 680	Leu	Ala	Ala	Val	Arg 685	Leu	Trp	Leu	Arg	Arg 690
Tyr	Gly	Asn	Leu	Lys 695	Ser	Pro	Glu	Pro	Pro 700	Met	Leu	Phe	Val	Arg 705
Trp	Gly	Leu	Pro	Leu 710	Met	Ala	Leu	Gly	Thr 715	Ala	Ala	Tyr	Trp	Ala 720
Leu	Ala	Ser	Gly	Ala 725	Asp	Glu	Ala	Pro	Pro 730	Arg	Leu	Arg	Val	Leu 735
Val	Ser	Gly	Ala	Ser 740	Met	Val	Leu	Pro	Arg 745	Ala	Val	Ala	Gly	Leu 750
Ala	Ala	Ser	Gly	Leu 755	Ala	Leu	Leu	Leu	Trp 760	Lys	Pro	Val	Thr	Val 765
Leu	Val	Lys	Ala	Gly 770	Ala	Gly	Ala	Pro	Arg 775	Thr	Arg	Thr	Val	Leu 780
Thr	Pro	Phe	Ser	Gly	Pro	Pro	Thr	Ser	Gln	Ala	Asp	Leu	Asp	Tyr

				785						790					795
Val	Val	Pro	Gln	Ile	Tyr	Arg	His	Met	Gln	Glu	Glu	Phe	Arg	Gly	
				800					805					810	
Arg	Leu	Glu	Arg	Thr	Lys	Ser	Gln	Gly	Pro	Leu	Thr	Val	Ala	Ala	
				815					820					825	
Tyr	Gln	Leu	Gly	Ser	Val	Tyr	Ser	Ala	Ala	Met	Val	Thr	Ala	Leu	
				830					835					840	
Thr	Leu	Leu	Ala	Phe	Pro	Leu	Leu	Leu	Leu	His	Ala	Glu	Arg	Ile	
				845					850					855	
Ser	Leu	Val	Phe	Leu	Leu	Leu	Phe	Leu	Gln	Ser	Phe	Leu	Leu	Leu	
				860					865					870	
His	Leu	Leu	Ala	Ala	Gly	Ile	Pro	Val	Thr	Thr	Pro	Gly	Pro	Phe	
				875					880					885	
Thr	Val	Pro	Trp	Gln	Ala	Val	Ser	Ala	Trp	Ala	Leu	Met	Ala	Thr	
				890					895					900	
Gln	Thr	Phe	Tyr	Ser	Thr	Gly	His	Gln	Pro	Val	Phe	Pro	Ala	Ile	
				905					910					915	
His	Trp	His	Ala	Ala	Phe	Val	Gly	Phe	Pro	Glu	Gly	His	Gly	Ser	
				920					925					930	
Cys	Thr	Trp	Leu	Pro	Ala	Leu	Leu	Val	Gly	Ala	Asn	Thr	Phe	Ala	
				935					940					945	
Ser	His	Leu	Leu	Phe	Ala	Val	Gly	Cys	Pro	Leu	Leu	Leu	Leu	Trp	
				950					955					960	
Pro	Phe	Leu	Cys	Glu	Ser	Gln	Gly	Leu	Arg	Lys	Arg	Gln	Gln	Pro	
				965					970					975	
Pro	Gly	Asn	Glu	Ala	Asp	Ala	Arg	Val	Arg	Pro	Glu	Glu	Glu	Glu	
				980					985					990	
Glu	Pro	Leu	Met	Glu	Met	Arg	Leu	Arg	Asp	Ala	Pro	Gln	His	Phe	
				995					1000					1005	
Tyr	Ala	Ala	Leu	Leu	Gln	Leu	Gly	Leu	Lys	Tyr	Leu	Phe	Ile	Leu	
				1010					1015					1020	
Gly	Ile	Gln	Ile	Leu	Ala	Cys	Ala	Leu	Ala	Ala	Ser	Ile	Leu	Arg	
				1025					1030					1035	
Arg	His	Leu	Met	Val	Trp	Lys	Val	Phe	Ala	Pro	Lys	Phe	Ile	Phe	
				1040					1045					1050	
Glu	Ala	Val	Gly	Phe	Ile	Val	Ser	Ser	Val	Gly	Leu	Leu	Leu	Gly	
				1055					1060					1065	
Ile	Ala	Leu	Val	Met	Arg	Val	Asp	Gly	Ala	Val	Ser	Ser	Trp	Phe	
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Arg Gln Leu Phe Leu Ala Gln Gln Arg
1085

<210> 103

<211> 1743

<212> DNA

<213> Homo sapiens

<400> 103

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cttatccatc aacatgaaga atgtcctaca atggactcca ccagaggggtc 150
ttcaaggagt taaagttact tacactgtgc agtatttcat cacaaattgg 200
cccaccagag gtggcactga ctacagatga gaagtccatt tctgttgctc 250
tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgtttcc 300
atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tgttgaatac 350
taaatcaaac agaacgtggg cccagtgtgt gaccaaccac acgctgggtg 400
tcacctggct ggagccgaac actctttact gcgtacacgt ggagtccttc 450
gtcccagggc cccctcgccg tgctcagcct tctgagaagc agtgtgccag 500
gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggt 550
atgttttgcc catatctatt accgtgtttc ttttttctgt gatgggctat 600
tccatctacc gatatatcca cgttggcaaa gagaaacacc cagcaaattt 650
gattttgatt tatggaaatg aatttgacaa aagattcttt gtgcctgctg 700
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atttctcatc aggatatgag ttactggga aaaagcagtg atgtatccag 800
ccttaatgat cctcagccca gcggaacct gaggccccct caggaggaag 850
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caggaggagg tgtccacaca aggaacatta ttggagtcgc aggcagcgtt 1100
ggcagtcttg ggcccgcaaa cgttacagta ctcatacacc cctcagctcc 1150
aagacttaga cccctggcg caggagcaca cagactcgga ggaggggccg 1200
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gctgtgtatt ccttcgctgt ccagcttcga ccaggattca gagggctgcg 1300
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 tatgaggagc cggtccaga caggccacca ggagaaaatg aaacctatct 1400
 catgcaattc atggaggaat ggggggtata tgtgcagatg gaaaactgat 1450
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 cgtgtgtgat tggttcatgc atgtaggctt cttacaatg atgggtgggc 1650
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 aaatgtttgc cagactgggt gcagaattta ttcaggtggg tgt 1743

<210> 104
 <211> 442
 <212> PRT
 <213> Homo sapiens

<400> 104
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 35 40 45
 Ala Pro Glu Lys Trp Lys Arg Asn Pro Glu Asp Leu Pro Val Ser
 50 55 60
 Met Gln Gln Ile Tyr Ser Asn Leu Lys Tyr Asn Val Ser Val Leu
 65 70 75
 Asn Thr Lys Ser Asn Arg Thr Trp Ser Gln Cys Val Thr Asn His
 80 85 90
 Thr Leu Val Leu Thr Trp Leu Glu Pro Asn Thr Leu Tyr Cys Val
 95 100 105
 His Val Glu Ser Phe Val Pro Gly Pro Pro Arg Arg Ala Gln Pro
 110 115 120
 Ser Glu Lys Gln Cys Ala Arg Thr Leu Lys Asp Gln Ser Ser Glu
 125 130 135
 Phe Lys Ala Lys Ile Ile Phe Trp Tyr Val Leu Pro Ile Ser Ile
 140 145 150
 Thr Val Phe Leu Phe Ser Val Met Gly Tyr Ser Ile Tyr Arg Tyr
 155 160 165

Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile	170	175	180
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys	185	190	195
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys	200	205	210
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val	215	220	225
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro	230	235	240
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu	245	250	255
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser	260	265	270
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys	275	280	285
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys	290	295	300
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser	305	310	315
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu	320	325	330
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp	335	340	345
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro	350	355	360
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr	365	370	375
Gly	Arg	Leu	Cys	Ile	Pro	Ser	Leu	Ser	Ser	Phe	Asp	Gln	Asp	Ser	380	385	390
Glu	Gly	Cys	Glu	Pro	Ser	Glu	Gly	Asp	Gly	Leu	Gly	Glu	Glu	Gly	395	400	405
Leu	Leu	Ser	Arg	Leu	Tyr	Glu	Glu	Pro	Ala	Pro	Asp	Arg	Pro	Pro	410	415	420
Gly	Glu	Asn	Glu	Thr	Tyr	Leu	Met	Gln	Phe	Met	Glu	Glu	Trp	Gly	425	430	435
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<210> 105

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<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct

<400> 105
    cgctgctgct gttgctcctg g 21

<210> 106
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 106
    cagtgtgcca ggactttg 18

<210> 107
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 107
    agtcgcaggc agcgttgg 18

<210> 108
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 108
    ctccctccgag tctgtgtgct cctgc 25

<210> 109
<211> 51
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence

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<222> 1-51
<223> Synthetic construct.

<400> 109
ggacgggcag ttccctgtgt ctctggtggt ttgcctaaac ctgcaaacat 50
c 51

<210> 110
<211> 1114
<212> DNA
<213> Homo sapiens

<400> 110
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tctgctgact gtggccaccg cctgatgct gcccgtaag cccccgcag 150
gctcctgggg ggcccagatc atcgggggcc acgaggtgac cccccactcc 200
aggccctaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250
cttcctgctg cgagcccgtt ggggtggtct ggccgcccac tgcttcagcc 300
acagagacct ccgcaactgg ctggtggtgc tgggcgcca cgtcctgagt 350
actgcggagc ccacccagca ggtgtttggc atcgatgctc tcaccacgca 400
ccccgactac cccccatga ccacgcca cgacatctgc ctgctgcggc 450
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aaaaaaaaaa gaaa 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

Met	Gly	Leu	Gly	Leu	Arg	Gly	Trp	Gly	Arg	Pro	Leu	Leu	Thr	Val
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Ala	Thr	Ala	Leu	Met	Leu	Pro	Val	Lys	Pro	Pro	Ala	Gly	Ser	Trp
				20					25					30

Gly	Ala	Gln	Ile	Ile	Gly	Gly	His	Glu	Val	Thr	Pro	His	Ser	Arg
				35					40					45

Pro	Tyr	Met	Ala	Ser	Val	Arg	Phe	Gly	Gly	Gln	His	His	Cys	Gly
				50					55					60

Gly	Phe	Leu	Leu	Arg	Ala	Arg	Trp	Val	Val	Ser	Ala	Ala	His	Cys
				65					70					75

Phe	Ser	His	Arg	Asp	Leu	Arg	Thr	Gly	Leu	Val	Val	Leu	Gly	Ala
				80					85					90

His	Val	Leu	Ser	Thr	Ala	Glu	Pro	Thr	Gln	Gln	Val	Phe	Gly	Ile
				95					100					105

Asp	Ala	Leu	Thr	Thr	His	Pro	Asp	Tyr	His	Pro	Met	Thr	His	Ala
				110					115					120

Asn	Asp	Ile	Cys	Leu	Leu	Arg	Leu	Asn	Gly	Ser	Ala	Val	Leu	Gly
				125					130					135

Pro	Ala	Val	Gly	Leu	Leu	Arg	Leu	Pro	Gly	Arg	Arg	Ala	Arg	Pro
				140					145					150

Pro	Thr	Ala	Gly	Thr	Arg	Cys	Arg	Val	Ala	Gly	Trp	Gly	Phe	Val
				155					160					165

Ser	Asp	Phe	Glu	Glu	Leu	Pro	Pro	Gly	Leu	Met	Glu	Ala	Lys	Val
				170					175					180

Arg	Val	Leu	Asp	Pro	Asp	Val	Cys	Asn	Ser	Ser	Trp	Lys	Gly	His
				185					190					195

Leu	Thr	Leu	Thr	Met	Leu	Cys	Thr	Arg	Ser	Gly	Asp	Ser	His	Arg
				200					205					210

Arg	Gly	Phe	Cys	Ser	Ala	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Arg
				215					220					225

Asn	Arg	Ala	His	Gly	Leu	Val	Ser	Phe	Ser	Gly	Leu	Trp	Cys	Gly
				230					235					240

Asp	Pro	Lys	Thr	Pro	Asp	Val	Tyr	Thr	Gln	Val	Ser	Ala	Phe	Val
				245					250					255

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly
 260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala
 275 280

<210> 112
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 112
 gacgtctgca acagctcctg gaag 24

<210> 113
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 113
 cgagaaggaa acgaggccgt gag 23

<210> 114
 <211> 44
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-44
 <223> Synthetic construct.

<400> 114
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<210> 115
 <211> 1808
 <212> DNA
 <213> Homo sapiens

<400> 115
 gagctaccca ggcggctggt gtgcagcaag ctccgcgccg actccggacg 50
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 tatgtcaccg gtggggcttg cccagcaag gccaccatcc ctgggaagac 200

ggatcatcgtg acgggcgcca acacaggcat cggaagcag accgccttgg 250
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 aagtgtgagg cggcagcaaa ggacatccgc ggggagacc tcaatcacca 350
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 gctcattt 1808

<210> 116
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 116
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 20 25 30
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 35 40 45
 Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg
 50 55 60
 Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys
 65 70 75
 Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His
 80 85 90
 Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg
 95 100 105
 Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile
 110 115 120
 Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr
 125 130 135
 Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His
 140 145 150
 Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala
 155 160 165
 Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly
 170 175 180
 His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn
 185 190 195
 Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe
 200 205 210
 Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val
 215 220 225

Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His
				230						235				240
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro
				245					250					255
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro
				260					265					270
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly
				275					280					285
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala
				290					295					300
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg
				305					310					315
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro
				320					325					330

Arg

<210> 117
 <211> 2249
 <212> DNA
 <213> Homo sapiens

<400> 117
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 gggcgacacg ttctcggcgc tgaccagcgt ggcgcgcgcc ctggcgcccc 150
 agcgccggct gctggggctg ctgaggcgtt acctgcgcgg ggaggaggcg 200
 cggtgcggg acctgaactag attctacgac aaggtacttt ctttgcata 250
 ggattcaaca acccctgtgg ctaaccctct gcttgcatct actctcatca 300
 aacgcctgca gtctgaactg aggaatgtgg tacatagtct ggaggccagt 350
 gagaacatcc gagctctgaa ggatggctat gagaagggtg agcaagacct 400
 tccagccttt gaggaccttg agggagcagc aagggccctg atgcggctgc 450
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 agagtcaactg gctctgccat cactgacctg tacagcccca aacggctctt 550
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 ttccaacgcc tacctgctgc tccagcccat ccggaaggag gtcattccacc 1050
 tggagcccta cattgctctc taccatgact tcgtcagtga ctcagaggct 1100
 cagaaaatta gagaacttgc agaaccatgg ctacagaggc cagtgggtggc 1150
 atcaggggag aagcagttac aagtggagta ccgcatcagc aaaagtgcct 1200
 ggctgaagga cactgttgac caaaaactgg tgaccctcaa ccaccgcatt 1250
 gctgccctca caggccttga tgtccggcct ccctatgcag agtatctgca 1300
 ggtggtgaac tatggcatcg gaggacacta tgagcctcac tttgaccatg 1350
 ctacgtcacc aagcagcccc ctctacagaa tgaagtcagg aaaccgagtt 1400
 gcaacattta tgatctatct gagctcgggtg gaagctggag gagccacagc 1450
 cttcatctat gccaacctca gcgtgcctgt ggtaggaat gcagcaactgt 1500
 tttggtggaa cctgcacagg agtgggtgaag gggacagtga cacacttcat 1550
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 acatgagtat ggacaggaat tccgcagacc ctgcagctcc agccctgaag 1650
 actgaactgt tggcagagag aagctgggtg agtcctgtgg ctttccagag 1700
 aagccaggag ccaaaagctg gggtaggaga ggagaaagca gagcagcctc 1750
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 gggagagggtt gttaccaggg gacactgaga atgtacattt gatctgcccc 1850
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 ggctgagag ggaagtttct ggagttcaga tactctctgt tgggaacagg 1950
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 cttgaccaca gggaccaaga agtggcaatg aggacacctg caggaggggc 2050
 tagcctgact cccagaactt taagactttc tccccactgc cttctgctgc 2100
 agcccaagca gggagtgtcc ccctcccaga agcatatccc agatgagtgg 2150

tacattatat aaggattttt ttttaagttga aaacaacttt cttttctttt 2200

tgtatgatgg tttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met Gly Pro Gly Ala Arg Leu Ala Ala Leu Leu Ala Val Leu Ala
1 5 10 15

Leu Gly Thr Gly Asp Pro Glu Arg Ala Ala Arg Gly Asp Thr
20 25 30

Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg
35 40 45

Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala
50 55 60

Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu
65 70 75

His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe
80 85 90

Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His
95 100 105

Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr
110 115 120

Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly
125 130 135

Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn
140 145 150

Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser
155 160 165

Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr
170 175 180

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly
185 190 195

Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu
200 205 210

Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser
215 220 225

Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala
230 235 240

530

535

540

Ser Pro Glu Asp

<210> 119

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 119

cgggacagga gacccagaaa ggg 23

<210> 120

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 120

ggccaagtga tccaaggcat cttc 24

<210> 121

<211> 49

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-49

<223> Synthetic construct.

<400> 121

ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcattgggg 49

<210> 122

<211> 1778

<212> DNA

<213> Homo sapiens

<400> 122

gagataggga gtctgggttt aagttcctgc tccatctcag gagcccctgc 50

tcccacccct aggaagccac cagactccac ggtgtggggc caatcagggtg 100

gaatcggccc tggcagggtg ggccacgagc gctggctgag ggaccgagcc 150

ggagagcccc ggagcccccg taaccgcgc ggggagcgcc caggatgccg 200

cgcggggact cggagcaggt gcgctactgc gcgcgcttct cctacctctg 250
 gctcaagttt tcaattatca tctattccac cgtgttctgg ctgattgggg 300
 ccctggtcct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350
 aaaaccottg aaagtgcctt cctggctcca gccatcatcc tcatcctcct 400
 gggcgtcgtc atgttcatgg tctccttcat tgggtgtgctg gcgtccctcc 450
 gtgacaacct gtaccttctc caagcattca tgtacatcct tgggatctgc 500
 ctcatcatgg agctcattgg tggcgtgggt gccttgacct tccggaacca 550
 gaccattgac ttctgaacg acaacattcg aagaggaatt gagaactact 600
 atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagttc 650
 aagtgtgtg gcggggagga ctaccgagat tggagcaaga atcagtacca 700
 cgactgcagt gcccctggac ccctggcctg tgggggtgcc tacacctgct 750
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 gcatcctcct gggcatcctg cttccccagt tcttgggggt gctgctgacg 950
 ctgctgtaca tcaccgggt ggaggacatc atcatggagc actctgtcac 1000
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 gctgtgtgtg cctgtgtgta ggtccacagg cctctgcctc cccagggagc 1250
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 tccttgagcc tagttttttt ttacgtgatt tttgtaacat tcattttttt 1650

gtacagataa caggagtttc tgactaatca aagctggtat ttccccgcat 1700
 gtcttattct tgcccttccc ccaaccagtt tgттаатcaa асаатааааа 1750
 catgttttgt tttgttttta аааааааа 1778

<210> 123
 <211> 294
 <212> PRT
 <213> Homo sapiens

<400> 123
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 1 5 10 15
 Ser Tyr Leu Trp Leu Lys Phe Ser Leu Ile Ile Tyr Ser Thr Val
 20 25 30
 Phe Trp Leu Ile Gly Ala Leu Val Leu Ser Val Gly Ile Tyr Ala
 35 40 45
 Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu
 50 55 60
 Ala Pro Ala Ile Ile Leu Ile Leu Leu Gly Val Val Met Phe Met
 65 70 75
 Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr
 80 85 90
 Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met
 95 100 105
 Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr
 110 115 120
 Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr
 125 130 135
 Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys
 140 145 150
 Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys
 155 160 165
 Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly
 170 175 180
 Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn
 185 190 195
 Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val
 200 205 210
 Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile
 215 220 225
 Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly

	230		235		240									
Ile	Leu	Leu	Pro	Gln	Phe	Leu	Gly	Val	Leu	Leu	Thr	Leu	Leu	Tyr
				245					250					255
Ile	Thr	Arg	Val	Glu	Asp	Ile	Ile	Met	Glu	His	Ser	Val	Thr	Asp
				260					265					270
Gly	Leu	Leu	Gly	Pro	Gly	Ala	Lys	Pro	Ser	Val	Glu	Ala	Ala	Gly
				275					280					285
Thr	Gly	Cys	Cys	Leu	Cys	Tyr	Pro	Asn						
				290										

<210> 124
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 124
 atcatctatt ccaccgtgtt ctggc 25

<210> 125
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 125
 gacagagtgc tccatgatga tgtcc 25

<210> 126
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 126
 cctgtctgtg ggcatttatg cagaggttga gcggcagaaa tataaaaccc 50

<210> 127
 <211> 1636
 <212> DNA
 <213> Homo sapiens

<400> 127

gaggagcggg ccgaggactc cagcgtgccc aggtctggca tcctgcactt 50
gctgccctct gacacctggg aagatggcog gcccggtggac cttcaccctt 100
ctctgtgggt tgctggcagc caccttgatc caagccaccc tcagtccac 150
tgcagttctc atcctcggcc caaaagtcat caaagaaaag ctgacacagg 200
agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250
agtgccatgc gggaaaagcc agcoggagge atccctgtgc tgggcagcct 300
ggtgaacacc gtcctgaagc acatcatctg gctgaaggtc atcacagcta 350
acatcctcca gctgcagggt aagccctcgg ccaatgacca ggagctgcta 400
gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctggtcaa 450
gaccatcgtg gagttccaca tgacgactga ggccaagcc accatccgca 500
tggacaccag tgcaagtggc cccaccogcc tggtcctcag tgactgtgcc 550
accagccatg ggagcctgcg catccaactg ctgtataagc tctccttcct 600
ggtgaacgcc ttagctaagc aggtcatgaa cctcctagtg ccatccctgc 650
ccaatctagt gaaaaaccag ctgtgtcccg tgatcgaggc ttccttcaat 700
ggcatgtatg cagacctcct gcagctggtg aagggtgcca tttccctcag 750
cattgaccgt ctggagtttg accttctgta tcctgccatc aagggtgaca 800
ccattcagct ctacctgggg gccaaagtgt tggactcaca gggaaagggtg 850
accaagtggg tcaataactc tgcagcttcc ctgacaatgc ccaccctgga 900
caacatcccg ttcagcctca tcgtgagtca ggacgtggtg aaagctgcag 950
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gaaacccagc tctcctgtct cccagtgaag acttggatgg cagccatcag 1550
ggaaggctgg gtcccagctg ggagtatggg tgtgagctct atagaccatc 1600
cctctctgca atcaataaac acttgccctgt gaaaaa 1636

<210> 128

<211> 484

<212> PRT

<213> Homo sapiens

<400> 128

Met	Ala	Gly	Pro	Trp	Thr	Phe	Thr	Leu	Leu	Cys	Gly	Leu	Leu	Ala
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Ala	Thr	Leu	Ile	Gln	Ala	Thr	Leu	Ser	Pro	Thr	Ala	Val	Leu	Ile
			20					25						30
Leu	Gly	Pro	Lys	Val	Ile	Lys	Glu	Lys	Leu	Thr	Gln	Glu	Leu	Lys
			35					40						45
Asp	His	Asn	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	Leu	Leu	Ser
			50					55						60
Ala	Met	Arg	Glu	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	Gly	Ser
			65					70						75
Leu	Val	Asn	Thr	Val	Leu	Lys	His	Ile	Ile	Trp	Leu	Lys	Val	Ile
			80					85						90
Thr	Ala	Asn	Ile	Leu	Gln	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp
			95					100						105
Gln	Glu	Leu	Leu	Val	Lys	Ile	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe
			110					115						120
Asn	Thr	Pro	Leu	Val	Lys	Thr	Ile	Val	Glu	Phe	His	Met	Thr	Thr
			125					130						135
Glu	Ala	Gln	Ala	Thr	Ile	Arg	Met	Asp	Thr	Ser	Ala	Ser	Gly	Pro
			140					145						150
Thr	Arg	Leu	Val	Leu	Ser	Asp	Cys	Ala	Thr	Ser	His	Gly	Ser	Leu
			155					160						165
Arg	Ile	Gln	Leu	Leu	Tyr	Lys	Leu	Ser	Phe	Leu	Val	Asn	Ala	Leu
			170					175						180
Ala	Lys	Gln	Val	Met	Asn	Leu	Leu	Val	Pro	Ser	Leu	Pro	Asn	Leu
			185					190						195
Val	Lys	Asn	Gln	Leu	Cys	Pro	Val	Ile	Glu	Ala	Ser	Phe	Asn	Gly
			200					205						210
Met	Tyr	Ala	Asp	Leu	Leu	Gln	Leu	Val	Lys	Val	Pro	Ile	Ser	Leu
			215					220						225

Ser	Ile	Asp	Arg	Leu	Glu	Phe	Asp	Leu	Leu	Tyr	Pro	Ala	Ile	Lys	230	235	240
Gly	Asp	Thr	Ile	Gln	Leu	Tyr	Leu	Gly	Ala	Lys	Leu	Leu	Asp	Ser	245	250	255
Gln	Gly	Lys	Val	Thr	Lys	Trp	Phe	Asn	Asn	Ser	Ala	Ala	Ser	Leu	260	265	270
Thr	Met	Pro	Thr	Leu	Asp	Asn	Ile	Pro	Phe	Ser	Leu	Ile	Val	Ser	275	280	285
Gln	Asp	Val	Val	Lys	Ala	Ala	Val	Ala	Ala	Val	Leu	Ser	Pro	Glu	290	295	300
Glu	Phe	Met	Val	Leu	Leu	Asp	Ser	Val	Leu	Pro	Glu	Ser	Ala	His	305	310	315
Arg	Leu	Lys	Ser	Ser	Ile	Gly	Leu	Ile	Asn	Glu	Lys	Ala	Ala	Asp	320	325	330
Lys	Leu	Gly	Ser	Thr	Gln	Ile	Val	Lys	Ile	Leu	Thr	Gln	Asp	Thr	335	340	345
Pro	Glu	Phe	Phe	Ile	Asp	Gln	Gly	His	Ala	Lys	Val	Ala	Gln	Leu	350	355	360
Ile	Val	Leu	Glu	Val	Phe	Pro	Ser	Ser	Glu	Ala	Leu	Arg	Pro	Leu	365	370	375
Phe	Thr	Leu	Gly	Ile	Glu	Ala	Ser	Ser	Glu	Ala	Gln	Phe	Tyr	Thr	380	385	390
Lys	Gly	Asp	Gln	Leu	Ile	Leu	Asn	Leu	Asn	Asn	Ile	Ser	Ser	Asp	395	400	405
Arg	Ile	Gln	Leu	Met	Asn	Ser	Gly	Ile	Gly	Trp	Phe	Gln	Pro	Asp	410	415	420
Val	Leu	Lys	Asn	Ile	Ile	Thr	Glu	Ile	Ile	His	Ser	Ile	Leu	Leu	425	430	435
Pro	Asn	Gln	Asn	Gly	Lys	Leu	Arg	Ser	Gly	Val	Pro	Val	Ser	Leu	440	445	450
Val	Lys	Ala	Leu	Gly	Phe	Glu	Ala	Ala	Glu	Ser	Ser	Leu	Thr	Lys	455	460	465
Asp	Ala	Leu	Val	Leu	Thr	Pro	Ala	Ser	Leu	Trp	Lys	Pro	Ser	Ser	470	475	480
Pro	Val	Ser	Gln														

<210> 129
 <211> 2213
 <212> DNA
 <213> Homo sapiens

<400> 129

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ctaacaaaag acctgtaata agaataaatg gagacaagtt ccgtcgcctt 200
gtgaaagccc caccgagaaa ttactccgtt atcgtcatgt tcaactgctct 250
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agatcctggc aaactcctgg cgatactcca gtgcattcac caacaggata 350
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ccaaacgggg tgatacatat gagttacagg tgcgggggtt ttcatgctgag 500
cagattgccc ggtggatcgc cgacagaact gatgtcaata ttagagtgat 550
tagaccccca aattatgctg gtccccttat gttgggattg cttttggctg 600
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aataaaaactg gatgggcttt tgcagctttg tgttttgtgc ttgctatgac 700
atctggtcaa atgtggaacc atataagagg accaccatat gcccataaga 750
atccccacac gggacatgtg aattatatcc atggaagcag tcaagcccag 800
ttttagactg aaacacacat tgttcttctg tttaatggtg gagttacctt 850
aggaatggtg cttttatgtg aagctgctac ctctgacatg gatattggaa 900
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aactactact ttgttttagt tagaacaag ctcaaaacta ctttagtta 1350
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 aaaaaaaaaa aaa 2213

<210> 130

<211> 335

<212> PRT

<213> Homo sapiens

<400> 130

Met	Ala	Ala	Arg	Trp	Arg	Phe	Trp	Cys	Val	Ser	Val	Thr	Met	Val
1				5					10				15	
Val	Ala	Leu	Leu	Ile	Val	Cys	Asp	Val	Pro	Ser	Ala	Ser	Ala	Gln
				20					25					30
Arg	Lys	Lys	Glu	Met	Val	Leu	Ser	Glu	Lys	Val	Ser	Gln	Leu	Met
				35					40					45
Glu	Trp	Thr	Asn	Lys	Arg	Pro	Val	Ile	Arg	Met	Asn	Gly	Asp	Lys
				50					55					60
Phe	Arg	Arg	Leu	Val	Lys	Ala	Pro	Pro	Arg	Asn	Tyr	Ser	Val	Ile
				65					70					75
Val	Met	Phe	Thr	Ala	Leu	Gln	Leu	His	Arg	Gln	Cys	Val	Val	Cys
				80					85					90
Lys	Gln	Ala	Asp	Glu	Glu	Phe	Gln	Ile	Leu	Ala	Asn	Ser	Trp	Arg
				95					100					105

Tyr	Ser	Ser	Ala	Phe	Thr	Asn	Arg	Ile	Phe	Phe	Ala	Met	Val	Asp	
				110					115					120	
Phe	Asp	Glu	Gly	Ser	Asp	Val	Phe	Gln	Met	Leu	Asn	Met	Asn	Ser	
				125					130					135	
Ala	Pro	Thr	Phe	Ile	Asn	Phe	Pro	Ala	Lys	Gly	Lys	Pro	Lys	Arg	
				140					145					150	
Gly	Asp	Thr	Tyr	Glu	Leu	Gln	Val	Arg	Gly	Phe	Ser	Ala	Glu	Gln	
				155					160					165	
Ile	Ala	Arg	Trp	Ile	Ala	Asp	Arg	Thr	Asp	Val	Asn	Ile	Arg	Val	
				170					175					180	
Ile	Arg	Pro	Pro	Asn	Tyr	Ala	Gly	Pro	Leu	Met	Leu	Gly	Leu	Leu	
				185					190					195	
Leu	Ala	Val	Ile	Gly	Gly	Leu	Val	Tyr	Leu	Arg	Arg	Ser	Asn	Met	
				200					205					210	
Glu	Phe	Leu	Phe	Asn	Lys	Thr	Gly	Trp	Ala	Phe	Ala	Ala	Leu	Cys	
				215					220					225	
Phe	Val	Leu	Ala	Met	Thr	Ser	Gly	Gln	Met	Trp	Asn	His	Ile	Arg	
				230					235					240	
Gly	Pro	Pro	Tyr	Ala	His	Lys	Asn	Pro	His	Thr	Gly	His	Val	Asn	
				245					250					255	
Tyr	Ile	His	Gly	Ser	Ser	Gln	Ala	Gln	Phe	Val	Ala	Glu	Thr	His	
				260					265					270	
Ile	Val	Leu	Leu	Phe	Asn	Gly	Gly	Val	Thr	Leu	Gly	Met	Val	Leu	
				275					280					285	
Leu	Cys	Glu	Ala	Ala	Thr	Ser	Asp	Met	Asp	Ile	Gly	Lys	Arg	Lys	
				290					295					300	
Ile	Met	Cys	Val	Ala	Gly	Ile	Gly	Leu	Val	Val	Leu	Phe	Phe	Ser	
				305					310					315	
Trp	Met	Leu	Ser	Ile	Phe	Arg	Ser	Lys	Tyr	His	Gly	Tyr	Pro	Tyr	
				320					325					330	
Ser	Phe	Leu	Met	Ser											
				335											

<210> 131
 <211> 2476
 <212> DNA
 <213> Homo sapiens

<400> 131
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cttggcgctg gcggtactgg cccccggagc aggggagcag aggcggagag 200
cagccaaagc gcccaatgtg gtgctggctg tgagcgactc cttcgatgga 250
aggttaacat ttcattccagg aagtcaggta gtgaaacttc cttttatcaa 300
ctttatgaag acacgtggga cttcctttct gaatgcctac acaaactctc 350
caatttggtg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400
ttaacagaat cttggaataa ttttaagggt ctagatccaa attatacaac 450
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aactggacta tacttcagga catcactcca ttagtaatcg tgtggaagcg 550
tggacaagag atgttgcttt cttactcaga caagaaggca ggcccatggg 600
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agaatacaga caaagcagta aactgggtta gaaaggaagc aattaattac 700
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tattttgtaa gaatgtagtg tattttaaga taaaatgcc aatgattataa 2200
aatcacatat ttcaaaaat gggtattatt taggcctttg tacaatttct 2250
aacaatttag tggaagtatc aaaaggattg aagcaaatac tgtaacagtt 2300
atgttccttt aaataataga gaatataaaa tattgtaata atatgtatca 2350
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<210> 132
<211> 536
<212> PRT
<213> Homo sapiens

<400> 132
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Val Leu Ala Pro Gly Ala Gly Glu Gln Arg Arg Arg Ala Ala Lys
20 25 30
Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg
35 40 45
Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile
50 55 60
Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr
65 70 75

Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly	
				80					85					90	
Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu	
				95					100					105	
Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly	
				110					115					120	
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His	
				125					130					135	
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala	
				140					145					150	
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg	
				155					160					165	
Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr	
				170					175					180	
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr	
				185					190					195	
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr	
				200					205					210	
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His	
				215					220					225	
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys	
				230					235					240	
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr	
				245					250					255	
Tyr	Ser	Ser	Tyr	Thr	Lys	Asn	Cys	Thr	Gly	Arg	Phe	Thr	Lys	Lys	
				260					265					270	
Glu	Ile	Lys	Asn	Ile	Arg	Ala	Phe	Tyr	Tyr	Ala	Met	Cys	Ala	Glu	
				275					280					285	
Thr	Asp	Ala	Met	Leu	Gly	Glu	Ile	Ile	Leu	Ala	Leu	His	Gln	Leu	
				290					295					300	
Asp	Leu	Leu	Gln	Lys	Thr	Ile	Val	Ile	Tyr	Ser	Ser	Asp	His	Gly	
				305					310					315	
Glu	Leu	Ala	Met	Glu	His	Arg	Gln	Phe	Tyr	Lys	Met	Ser	Met	Tyr	
				320					325					330	
Glu	Ala	Ser	Ala	His	Val	Pro	Leu	Leu	Met	Met	Gly	Pro	Gly	Ile	
				335					340					345	
Lys	Ala	Gly	Leu	Gln	Val	Ser	Asn	Val	Val	Ser	Leu	Val	Asp	Ile	
				350					355					360	
Tyr	Pro	Thr	Met	Leu	Asp	Ile	Ala	Gly	Ile	Pro	Leu	Pro	Gln	Asn	

	365		370		375
Leu Ser Gly Tyr	Ser 380	Leu Leu Pro Leu	Ser 385	Ser Glu Thr Phe	Lys 390
Asn Glu His Lys	Val 395	Lys Asn Leu His	Pro 400	Pro Trp Ile Leu	Ser 405
Glu Phe His Gly	Cys 410	Asn Val Asn Ala	Ser 415	Thr Tyr Met Leu	Arg 420
Thr Asn His Trp	Lys 425	Tyr Ile Ala Tyr	Ser 430	Asp Gly Ala Ser	Ile 435
Leu Pro Gln Leu	Phe 440	Asp Leu Ser Ser	Asp 445	Pro Asp Glu Leu	Thr 450
Asn Val Ala Val	Lys 455	Phe Pro Glu Ile	Thr 460	Tyr Ser Leu Asp	Gln 465
Lys Leu His Ser	Ile 470	Ile Asn Tyr Pro	Lys 475	Val Ser Ala Ser	Val 480
His Gln Tyr Asn	Lys 485	Glu Gln Phe Ile	Lys 490	Trp Lys Gln Ser	Ile 495
Gly Gln Asn Tyr	Ser 500	Asn Val Ile Ala	Asn 505	Leu Arg Trp His	Gln 510
Asp Trp Gln Lys	Glu 515	Pro Arg Lys Tyr	Glu 520	Asn Ala Ile Asp	Gln 525
Trp Leu Lys Thr	His 530	Met Asn Pro Arg	Ala 535	Val	

<210> 133
 <211> 1475
 <212> DNA
 <213> Homo sapiens

<400> 133
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 gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtggg 150
 ctacatccta ggccttctgg ggcttttggg cacactggtt gccatgctgc 200
 tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250
 gttggcttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300
 catcaccagc tgtgacatct atagcacctt tctgggcctg cccgctgaca 350
 tccaggctgc ccaggccatg atggtgacat ccagtgcaat ctccctccctg 400
 gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450

atctcccatc tccagtaa at gtgaaagcag aagacgtttt ccctgagaag 400
 acatagaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450
 aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550
 atgacagtag attatcagga aataaataaa gtgggtttttc caatgtacac 600
 acctgtaaaa 610

<210> 136
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 136
 Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu
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 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu
 20 25 30
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
 35 40 45
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
 50 55 60
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys
 65 70 75
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe
 80 85 90
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser
 95 100 105
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro
 110 115

<210> 137
 <211> 771
 <212> DNA
 <213> Homo sapiens

<400> 137
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 agtggccccc atgactcctt acctgatgct gtgccagcca cacaagagat 150
 gtggggacaa gttctacgac ccctgcagc actgttgcta tgatgatgcc 200
 gtcgtgccct tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250

ctgctttgag cagtgtctgcc cctggacctt catggtgaag ctgataaacc 300
agaactgcga ctcagcccg g acctcggatg acaggctttg tcgcagtgtc 350
agctaattgga acatcagggg aacgatgact cctggattct ccttcctggg 400
tgggcctgga gaaagaggct ggtgttacct gagatctggg atgctgagtg 450
gctgtttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500
gacctgtctg agggccaccc tgcagctgcc ctgaggaggc ccacaggtcc 550
ccttctagaa ttctggacag catgagatgc gtgtgctgat gggggcccag 600
ggactctgaa cctcctgat gaccctatg gccaacatca acccggcacc 650
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atctcaagtt ctcttctatc caggagcaaa gcacaggatc ataataaatt 750
tatgtacttt ataaatgaaa a 771

<210> 138

<211> 110

<212> PRT

<213> Homo sapiens

<400> 138

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Ile	Ser	Arg	Leu	Leu	Cys	Ser	His	Gly	Ala	Pro	Val	Ala	Pro	Met
			20					25						30

Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp
			35					40						45

Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val
			50					55						60

Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg
			65					70						75

Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu
			80					85						90

Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu
			95					100						105

Cys	Arg	Ser	Val	Ser
				110

<210> 139

<211> 2044

<212> DNA

<213> Homo sapiens

<400> 139

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 ctccccgga ccagaagttc ctctgcgcgt ccgacggcga catgggcgtc 150
 cccacggccc tggaggcgg cagctggcgc tggggatccc tgctcttcgc 200
 tctcttcctg gctgcgtccc taggtccggt ggcagccttc aaggtcgcca 250
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 gtcggcctcc gaccaccatg gcaacttctc catcaccatg cgcaacctga 550
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 ctcccactgc tcagcgcggg ccattgcaag ggtgccacac aatgtcttgt 1950
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 tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140

<211> 311

<212> PRT

<213> Homo sapiens

<400> 140

Met	Gly	Val	Pro	Thr	Ala	Leu	Glu	Ala	Gly	Ser	Trp	Arg	Trp	Gly
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Ser	Leu	Leu	Phe	Ala	Leu	Phe	Leu	Ala	Ala	Ser	Leu	Gly	Pro	Val
				20					25					30
Ala	Ala	Phe	Lys	Val	Ala	Thr	Pro	Tyr	Ser	Leu	Tyr	Val	Cys	Pro
				35					40					45
Glu	Gly	Gln	Asn	Val	Thr	Leu	Thr	Cys	Arg	Leu	Leu	Gly	Pro	Val
				50					55					60
Asp	Lys	Gly	His	Asp	Val	Thr	Phe	Tyr	Lys	Thr	Trp	Tyr	Arg	Ser
				65					70					75
Ser	Arg	Gly	Glu	Val	Gln	Thr	Cys	Ser	Glu	Arg	Arg	Pro	Ile	Arg
				80					85					90
Asn	Leu	Thr	Phe	Gln	Asp	Leu	His	Leu	His	His	Gly	Gly	His	Gln
				95					100					105
Ala	Ala	Asn	Thr	Ser	His	Asp	Leu	Ala	Gln	Arg	His	Gly	Leu	Glu
				110					115					120
Ser	Ala	Ser	Asp	His	His	Gly	Asn	Phe	Ser	Ile	Thr	Met	Arg	Asn
				125					130					135
Leu	Thr	Leu	Leu	Asp	Ser	Gly	Leu	Tyr	Cys	Cys	Leu	Val	Val	Glu

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cagcaatgct gtcccaagtg tgtggaacct cacactccct ctggactccg 600
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cagtcgctcc atggggtgag acatcctcag gatccatgtt ccagtgatgc 900
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ctctgagctt catccctcgc cacttcagac ccaagggagc aggcagcaca 1000
actgtcaaga tcgtcctgaa ggagaaacat aagaaagcct gtgtgcatgg 1050
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gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300
ctcgtccaca catcggtatc cccaagccca gacaacctgc gtcgctttgc 1350
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taaaagatga ggaaactgag gctcagagag gtgaagtacc tggcccaagg 1450
ccacacagcc agaatcttcc acttgactca gatcaagaaa gtcaggaagc 1500
aagacttcca gaaagaggca cagcacttcc gactgctcgc tggccccac 1550
gaaggtcact ggaacgtctt cctagcccag accctggagc tgaaggtcac 1600
ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650
gatatgagct gtataattgt tgttattata tattaataaa taagaagttg 1700
cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142
<211> 451
<212> PRT
<213> Homo sapiens
<400> 142

Met	Val	Pro	Glu	Val	Arg	Val	Leu	Ser	Ser	Leu	Leu	Gly	Leu	Ala	
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Leu	Leu	Trp	Phe	Pro	Leu	Asp	Ser	His	Ala	Arg	Ala	Arg	Pro	Asp	
				20					25					30	
Met	Phe	Cys	Leu	Phe	His	Gly	Lys	Arg	Tyr	Ser	Pro	Gly	Glu	Ser	
				35					40					45	
Trp	His	Pro	Tyr	Leu	Glu	Pro	Gln	Gly	Leu	Met	Tyr	Cys	Leu	Arg	
				50					55					60	
Cys	Thr	Cys	Ser	Glu	Gly	Ala	His	Val	Ser	Cys	Tyr	Arg	Leu	His	
				65					70					75	
Cys	Pro	Pro	Val	His	Cys	Pro	Gln	Pro	Val	Thr	Glu	Pro	Gln	Gln	
				80					85					90	
Cys	Cys	Pro	Lys	Cys	Val	Glu	Pro	His	Thr	Pro	Ser	Gly	Leu	Arg	
				95					100					105	
Ala	Pro	Pro	Lys	Ser	Cys	Gln	His	Asn	Gly	Thr	Met	Tyr	Gln	His	
				110					115					120	
Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro	
				125					130					135	
Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys	
				140					145					150	
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro	
				155					160					165	
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu	
				170					175					180	
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg	
				185					190					195	
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly	
				200					205					210	
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Phe	
				215					220					225	
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val	
				230					235					240	
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly	
				245					250					255	
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg	
				260					265					270	
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly	
				275					280					285	
Arg	Gln	Asp	Cys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Cys	

290	295	300
Arg His Pro Glu Lys Val Ala Gly Lys Cys Cys Lys Ile Cys Pro	305	310
Glu Asp Lys Ala Asp Pro Gly His Ser Glu Ile Ser Ser Thr Arg	320	325
Cys Pro Lys Ala Pro Gly Arg Val Leu Val His Thr Ser Val Ser	335	340
Pro Ser Pro Asp Asn Leu Arg Arg Phe Ala Leu Glu His Glu Ala	350	355
Ser Asp Leu Val Glu Ile Tyr Leu Trp Lys Leu Val Lys Asp Glu	365	370
Glu Thr Glu Ala Gln Arg Gly Glu Val Pro Gly Pro Arg Pro His	380	385
Ser Gln Asn Leu Pro Leu Asp Ser Asp Gln Glu Ser Gln Glu Ala	395	400
Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro	410	415
Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala	425	430
Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys	440	445

Thr

<210> 143
 <211> 693
 <212> DNA
 <213> Homo sapiens

<400> 143
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 cgaggagctc ccgtgggcgc tccgctggct gtgcaggcgg ccatggattc 100
 cttgcggaaa atgctgatct cagtcgcaat gctgggcgca ggggctggcg 150
 tgggctacgc gtcctcggtt atcgtgaccc cgggagagcg gcggaagcag 200
 gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250
 ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300
 cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350
 ggcgccagcg ggaggtcacc gtgagaccgg acttgccctc gtgggcgccg 400
 gaccttggct tgggcgcagg aatccgaggc agcctttctc cttcgtgggc 450

ccagcggaga gtccggaccg agataccatg ccaggactct ccggggtcct 500
 gtgagctgcc gtccgggtgag cacgtttccc ccaaaccctg gactgactgc 550
 tttaagggtcc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600
 aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 144
 Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly
 1 5 10 15
 Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro
 20 25 30
 Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln
 35 40 45
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
 50 55 60
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala
 65 70 75
 Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly
 80 85 90
 Arg Ser Pro

<210> 145
 <211> 1883
 <212> DNA
 <213> Homo sapiens

<400> 145
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 caggctgcca tggggcccag caccctctc ctcatcttgt tccttttgtc 150
 atggtcggga cccctccaag gacagcagca ccaccttggtg gactacatgg 200
 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250
 agtagtcggc atgctgctga gctgctggac ttcaagaaca agatgctgcc 300
 actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350
 acaccatctc cgggagagtg gatcgtcttg agcgggaggt agactatctg 400

gagacccaga acccagctct gccctgtgta gagtttgatg agaaggtgac 450
 tggaggccct gggaccaaag gcaagggaaag aaggaatgag aagtacgata 500
 tggtgacaga ctgtggctac acaatctctc aagtgagatc aatgaagatt 550
 ctgaagcgat ttggtggccc agctggtcta tggaccaagg atccactggg 600
 gcaaacagag aagatctacg tgtagatggg gacacagaat gacacagcct 650
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 aaccgaacag tgggtggacag ctcagtattc ccagcagagg ggctgatccc 900
 cccctacggc ttgacagcag acacctacat cgacctggta gctgatgagg 950
 aaggtctttg ggctgtctat gccacccggg aggatgacag gcacttgtgt 1000
 ctggccaagt tagatccaca gacactggac acagagcagc agtgggacac 1050
 accatgtccc agagagaatg ctgaggtgc ctttgtcatt tgtgggaccc 1100
 tctatgtcgt ctataacacc cgtcctgcca gtccgggccc catccagtgc 1150
 tcctttgatg ccagcggcac cctgaccctt gaacgggcag cactccctta 1200
 ttttccccgc agatatggtg cccatgccag cctccgctat aacccccgag 1250
 aacgccagct ctatgcctgg gatgatggct accagattgt ctataagctg 1300
 gagatgagga agaaagagga ggaggtttga ggagctagcc ttgttttttg 1350
 catctttctc actcccatc atttatatta tatccccact aaatttcttg 1400
 ttctcattc ttcaaagtgt ggccagttgt ggctcaaata ctctatattt 1450
 ttagccaatg gcaatcaaata tctttcagct cctttgtttc atacggaact 1500
 ccagatcctg agtaatcctt ttagagcccc aagagtcaaa accctcaatg 1550
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 cccagacca gggctctaac cttgtatgcg ggcaggccca gggagcaggc 1650
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 acgtccagct ctgtcctctc ttctcactc ctcccttcag tgtcctgagg 1750
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 gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met	Gly	Pro	Ser	Thr	Pro	Leu	Leu	Ile	Leu	Phe	Leu	Leu	Ser	Trp
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Ser	Gly	Pro	Leu	Gln	Gly	Gln	Gln	His	His	Leu	Val	Glu	Tyr	Met
				20					25					30
Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln
				35					40					45
Asp	Gln	Ser	Ser	Arg	His	Ala	Ala	Glu	Leu	Arg	Asp	Phe	Lys	Asn
				50					55					60
Lys	Met	Leu	Pro	Leu	Leu	Glu	Val	Ala	Glu	Lys	Glu	Arg	Glu	Ala
				65					70					75
Leu	Arg	Thr	Glu	Ala	Asp	Thr	Ile	Ser	Gly	Arg	Val	Asp	Arg	Leu
				80					85					90
Glu	Arg	Glu	Val	Asp	Tyr	Leu	Glu	Thr	Gln	Asn	Pro	Ala	Leu	Pro
				95					100					105
Cys	Val	Glu	Phe	Asp	Glu	Lys	Val	Thr	Gly	Gly	Pro	Gly	Thr	Lys
				110					115					120
Gly	Lys	Gly	Arg	Arg	Asn	Glu	Lys	Tyr	Asp	Met	Val	Thr	Asp	Cys
				125					130					135
Gly	Tyr	Thr	Ile	Ser	Gln	Val	Arg	Ser	Met	Lys	Ile	Leu	Lys	Arg
				140					145					150
Phe	Gly	Gly	Pro	Ala	Gly	Leu	Trp	Thr	Lys	Asp	Pro	Leu	Gly	Gln
				155					160					165
Thr	Glu	Lys	Ile	Tyr	Val	Leu	Asp	Gly	Thr	Gln	Asn	Asp	Thr	Ala
				170					175					180
Phe	Val	Phe	Pro	Arg	Leu	Arg	Asp	Phe	Thr	Leu	Ala	Met	Ala	Ala
				185					190					195
Arg	Lys	Ala	Ser	Arg	Val	Arg	Val	Pro	Phe	Pro	Trp	Val	Gly	Thr
				200					205					210
Gly	Gln	Leu	Val	Tyr	Gly	Gly	Phe	Leu	Tyr	Phe	Ala	Arg	Arg	Pro
				215					220					225
Pro	Gly	Arg	Pro	Gly	Gly	Gly	Gly	Glu	Met	Glu	Asn	Thr	Leu	Gln
				230					235					240
Leu	Ile	Lys	Phe	His	Leu	Ala	Asn	Arg	Thr	Val	Val	Asp	Ser	Ser
				245					250					255

Val	Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala	260	265	270
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala	275	280	285
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys	290	295	300
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro	305	310	315
Cys	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr	320	325	330
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile	335	340	345
Gln	Cys	Ser	Phe	Asp	Ala	Ser	Gly	Thr	Leu	Thr	Pro	Glu	Arg	Ala	350	355	360
Ala	Leu	Pro	Tyr	Phe	Pro	Arg	Arg	Tyr	Gly	Ala	His	Ala	Ser	Leu	365	370	375
Arg	Tyr	Asn	Pro	Arg	Glu	Arg	Gln	Leu	Tyr	Ala	Trp	Asp	Asp	Gly	380	385	390
Tyr	Gln	Ile	Val	Tyr	Lys	Leu	Glu	Met	Arg	Lys	Lys	Glu	Glu	Glu	395	400	405
Val																	

<210> 147
 <211> 2052
 <212> DNA
 <213> Homo sapiens

<400> 147
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 ccgctcacgc agagcctctc cgtggcttcc gcaccttgag cattaggcca 100
 gttctcctct tctctctaatt ccatccgtca cctctcctgt catccgtttc 150
 catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200
 ttggttctga gtctcctcaa gctgggatca gggcagtggc aggtgtttgg 250
 gccagacaag cctgtccagg ccttggtggg ggaggacgca gcattctcct 300
 gtttcctgtc tcctaagacc aatgcagagg ccatggaagt gcggttcttc 350
 aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400
 gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450
 attctattgc ggagggggcg atctctctga ggctggaaaa cattactgtg 500

ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca 550
 gaaggccatc tgggagctac aggtgtcagc actgggctca gttcctctca 600
 tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtcc 650
 tcgggctggt tcccccgcc cacagcgaag tggaaaggtc cacaaggaca 700
 ggatttgtcc acagactcca ggacaaacag agacatgcac ggctgtttg 750
 atgtggagat ctctctgacc gtccaagaga acgccgggag catatcctgt 800
 tccatgcggc atgctcatct gagccgagag gtggaatcca gggtagacat 850
 aggagatacc tttttcgagc ctatatcgtg gcacctggct accaaagtac 900
 tgggaatact ctgctgtggc ctattttttg gcattgttgg actgaagatt 950
 ttctttctca aattccagtg gaaaatccag gcggaactgg actggagaag 1000
 aaagcacgga caggcagaat tgagagacgc ccggaacac gcagtggagg 1050
 tgactctgga tccagagacg gctcaccgga agctctgcgt ttctgatctg 1100
 aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa 1150
 gagatttaca aggaagagtg tgggtggcttc tcagagtttc caagcaggga 1200
 aacattactg ggaggtggac ggaggacaca ataaaagggtg gcgcgtggga 1250
 gtgtgccggg atgatgtgga caggaggaag gagtacgtga ctttgtctcc 1300
 cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350
 cattaatcc ccgttttacc agcgtcttcc ccaggacccc acctacaaaa 1400
 ataggggtct tcctggacta tgagtgtggg accatctcct tcttcaacat 1450
 aaatgaccag tcccttattt ataccctgac atgtcgggtt gaaggcttat 1500
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 atagtcatct gccagtcac ccaggaatca gagaaagagg cctcttggca 1600
 aagggcctct gcaatcccag agacaagcaa cagtgagtcc tcctcacagg 1650
 caaccacgcc cttcctcccc aggggtgaaa tgtaggatga atcacatccc 1700
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 cagcagccgg ccaagggtggc ttccagatga agggggactg gcctgtccac 1800
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 cattacattt agtttgctct cactccatct ggctaagtga tcttgaaata 1900
 ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg 1950

tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000
acagagtgta tcctaatggt ttgttcatta tattacactt tcagtaaaaa 2050
aa 2052

<210> 148
<211> 500
<212> PRT
<213> Homo sapiens

<400> 148
Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly
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Ser Gly Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala
20 25 30
Leu Val Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys
35 40 45
Thr Asn Ala Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe
50 55 60
Ser Ser Val Val His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe
65 70 75
Met Gln Met Pro Gln Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp
80 85 90
Ser Ile Ala Glu Gly Arg Ile Ser Leu Arg Leu Glu Asn Ile Thr
95 100 105
Val Leu Asp Ala Gly Leu Tyr Gly Cys Arg Ile Ser Ser Gln Ser
110 115 120
Tyr Tyr Gln Lys Ala Ile Trp Glu Leu Gln Val Ser Ala Leu Gly
125 130 135
Ser Val Pro Leu Ile Ser Ile Thr Gly Tyr Val Asp Arg Asp Ile
140 145 150
Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe Pro Arg Pro Thr Ala
155 160 165
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Thr Asp Ser Arg
170 175 180
Thr Asn Arg Asp Met His Gly Leu Phe Asp Val Glu Ile Ser Leu
185 190 195
Thr Val Gln Glu Asn Ala Gly Ser Ile Ser Cys Ser Met Arg His
200 205 210
Ala His Leu Ser Arg Glu Val Glu Ser Arg Val Gln Ile Gly Asp
215 220 225
Thr Phe Phe Glu Pro Ile Ser Trp His Leu Ala Thr Lys Val Leu

	230		235		240
Gly Ile Leu Cys	Cys Gly Leu Phe Phe	Gly Ile Val Gly Leu Lys			
	245		250		255
Ile Phe Phe Ser	Lys Phe Gln Trp Lys	Ile Gln Ala Glu Leu Asp			
	260		265		270
Trp Arg Arg Lys	His Gly Gln Ala Glu	Leu Arg Asp Ala Arg Lys			
	275		280		285
His Ala Val Glu	Val Thr Leu Asp Pro	Glu Thr Ala His Pro Lys			
	290		295		300
Leu Cys Val Ser	Asp Leu Lys Thr Val	Thr His Arg Lys Ala Pro			
	305		310		315
Gln Glu Val Pro	His Ser Glu Lys Arg	Phe Thr Arg Lys Ser Val			
	320		325		330
Val Ala Ser Gln	Ser Phe Gln Ala Gly	Lys His Tyr Trp Glu Val			
	335		340		345
Asp Gly Gly His	Asn Lys Arg Trp Arg	Val Gly Val Cys Arg Asp			
	350		355		360
Asp Val Asp Arg	Arg Lys Glu Tyr Val	Thr Leu Ser Pro Asp His			
	365		370		375
Gly Tyr Trp Val	Leu Arg Leu Asn Gly	Glu His Leu Tyr Phe Thr			
	380		385		390
Leu Asn Pro Arg	Phe Ile Ser Val Phe	Pro Arg Thr Pro Pro Thr			
	395		400		405
Lys Ile Gly Val	Phe Leu Asp Tyr Glu	Cys Gly Thr Ile Ser Phe			
	410		415		420
Phe Asn Ile Asn	Asp Gln Ser Leu Ile	Tyr Thr Leu Thr Cys Arg			
	425		430		435
Phe Glu Gly Leu	Leu Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr Asn			
	440		445		450
Glu Gln Asn Gly	Thr Pro Ile Val Ile	Cys Pro Val Thr Gln Glu			
	455		460		465
Ser Glu Lys Glu	Ala Ser Trp Gln Arg	Ala Ser Ala Ile Pro Glu			
	470		475		480
Thr Ser Asn Ser	Glu Ser Ser Ser Gln	Ala Thr Thr Pro Phe Leu			
	485		490		495
Pro Arg Gly Glu	Met				
	500				

<210> 149
 <211> 24

<212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 149
 gcgtggtcca cctctacagg gacg 24

<210> 150
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 150
 ggaactgacc cagtgtgac acc 23

<210> 151
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 151
 gcagatgccca cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152
 <211> 2294
 <212> DNA
 <213> Homo sapiens

<400> 152
 gcgatggtgc gcccgggtggc ggtggcggcg gcggttgcg aggccttcctt 50
 ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100
 aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggcg 150
 gcctcgccct gttgtgctgc gccgcgcgcg ccgcgcgcgt cgcctcagcc 200
 gcctcggcgg ggaatgtcac cgggtggcggc ggggccgcgg ggcaggtgga 250
 cgcgtcgccg ggccccgggt tgcggggcga gccagccac cccttccta 300
 gggcgacggc tcccacggcc caggccccga ggaccgggccc cccgcgcgcc 350
 accgtccacc gacccctggc tgcgacttct ccagcccagt ccccgagac 400

cacccctctt tgggcgactg ctggaccctc ttccaccacc tttcaggcgc 450
cgctcggccc ctgcgcgacc acccctccgg cggcggaacg cacttcgacc 500
acctctcagg cgccgaccag acccgcgccg accacccttt cgacgaccac 550
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agaccacagg gcagtgtgag tgtcggccag gttatcaggg gcttcactgt 800
gaaacctgca aagagggtct ttacctaaat tacacttctg ggctctgtca 850
gccatgtgac tgtagtcac atggagctct cagcataccg tgcaacaggt 900
aagcaacaga ggggtggaact gaagtttatt ttatttttagc aagggaataa 950
aaaaggctgc tactctcaag gaccatactg gtttaaacaa aggaggatga 1000
gggtcataga ttacaaaat attttatata cttttattct cttactttat 1050
atgttatatt taatgtcagg atttaaaaac atctaattta ctgatttagt 1100
tcttcaaaag cactagagtc gccaatTTTT ctctgggata atttctgtaa 1150
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taatcaaat tctacatttg tttctttgga catctaaagc ttaacctggg 1350
ggtaccctaa tttatttaac tagtggttag tagactggtt ttactctatt 1400
taccagtaca tttttgagac caaaagtaga ttaagcagga attatcttta 1450
aactattatg ttatttgag gtaatttaat ctagtggaat aatgtactgt 1500
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acagtattaa ataataaaaa aaataatgac aggttatact cagtgttaacc 1650
tgggtataac ccaagatctg ctgccactta cgagctgtgt tccttgggca 1700
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ctggtttgtt ttaatttcaa aggaatatta tggactgaaa tgagagaaca 1850

tgttttaaga acttttagct ccttgacaaa gaagtgcttt atacttttagc 1900
 actaaatatt ttaaagtctt tataaatgat attatactgt tatggaatat 1950
 tgtatcatat tgtagtttat taaaaatgta gaagaggctg ggcgcggtgg 2000
 ctacgcctg taatcctagc actttgggag gccaaggcgg gtggatcact 2050
 tgaggccagg agttctagat gagcctggcc agcacagtga aaccccgctct 2100
 ctactaaaaa tacaacaaaa ttagctgggc gtggtggcac acacctgtag 2150
 tcccagctac tcgggaggct gaggcaggag aatcggttga acccgggagg 2200
 tggaggttgc agtgagctga gatcgcgcca ctgcactcca gcctggtgag 2250
 agaggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153
 <211> 258
 <212> PRT
 <213> Homo sapiens

<400> 153
 Met Arg Ser Leu Pro Ser Leu Gly Gly Leu Ala Leu Leu Cys Cys
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 20 25 30
 Val Thr Gly Gly Gly Gly Ala Ala Gly Gln Val Asp Ala Ser Pro
 35 40 45
 Gly Pro Gly Leu Arg Gly Glu Pro Ser His Pro Phe Pro Arg Ala
 50 55 60
 Thr Ala Pro Thr Ala Gln Ala Pro Arg Thr Gly Pro Pro Arg Ala
 65 70 75
 Thr Val His Arg Pro Leu Ala Ala Thr Ser Pro Ala Gln Ser Pro
 80 85 90
 Glu Thr Thr Pro Leu Trp Ala Thr Ala Gly Pro Ser Ser Thr Thr
 95 100 105
 Phe Gln Ala Pro Leu Gly Pro Ser Pro Thr Thr Pro Pro Ala Ala
 110 115 120
 Glu Arg Thr Ser Thr Thr Ser Gln Ala Pro Thr Arg Pro Ala Pro
 125 130 135
 Thr Thr Leu Ser Thr Thr Thr Gly Pro Ala Pro Thr Thr Pro Val
 140 145 150
 Ala Thr Thr Val Pro Ala Pro Thr Thr Pro Arg Thr Pro Thr Pro
 155 160 165
 Asp Leu Pro Ser Ser Ser Asn Ser Ser Val Leu Pro Thr Pro Pro

170										175					180				
Ala	Thr	Glu	Ala	Pro	Ser	Ser	Pro	Pro	Pro	Glu	Tyr	Val	Cys	Asn					
				185					190					195					
Cys	Ser	Val	Val	Gly	Ser	Leu	Asn	Val	Asn	Arg	Cys	Asn	Gln	Thr					
				200					205					210					
Thr	Gly	Gln	Cys	Glu	Cys	Arg	Pro	Gly	Tyr	Gln	Gly	Leu	His	Cys					
				215					220					225					
Glu	Thr	Cys	Lys	Glu	Gly	Phe	Tyr	Leu	Asn	Tyr	Thr	Ser	Gly	Leu					
				230					235					240					
Cys	Gln	Pro	Cys	Asp	Cys	Ser	Pro	His	Gly	Ala	Leu	Ser	Ile	Pro					
				245					250					255					

Cys Asn Arg

<210> 154
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 154
 aactgctctg tggttgaag cctg 24

<210> 155
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 155
 cagtcacatg gctgacagac ccac 24

<210> 156
 <211> 38
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-38
 <223> Synthetic construct.

<400> 156
 aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157
 <211> 689
 <212> DNA
 <213> Homo sapiens

<400> 157
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 ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggtggcctc 150
 ccgggaaaag ggctttgcc aaggagaagga catgaagaac gtcgtggggg 200
 tgggtgtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250
 cacgggctgg gaggggtgtga ccagagtgtc atggacctga taaagcgaaa 300
 ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350
 tgctggccac caacttcaga gactatgcc aatctctcac tcagctggag 400
 ttcggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450
 agccagccag gagggcatgg ggctcttcac caagtggagc aggagcctgg 500
 gcttcctgtc acagtagcag gccagctgc agaaggacct cacctgtgct 550
 cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgccaca 600
 gggtcctgtg acctcgcca gtgtccccc acctcgctca gcggctcccg 650
 gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 158
 Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val
 1 5 10 15
 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln
 20 25 30
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
 35 40 45
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
 50 55 60
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
 65 70 75
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
 80 85 90

Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
				95					100					105
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile
				110					115					120
Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu
				125					130					135
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu
				140					145					150
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln		
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<210> 159

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 159

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gtaaactgct gacgatgcag agttccgtga cgggtgcagga aggcctgtgt 150
gtccatgtgc cctgctcctt ctccatcccc tcgcatggct ggatttaccc 200
tggcccagta gttcatggct actggttccg ggaagggggc aatacagacc 250
aggatgctcc agtggccaca aacaacccag ctcgggcagt gtgggaggag 300
actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350
cctgagcatc agagatgcc aagaagtga tgcggggaga tacttctttc 400
gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450
gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500
cctggagtcc ggctgcccc agaatctgac ctgctctgtg ccctgggcct 550
gtgagcaggg gacaccccct atgatctcct ggatagggac ctccgtgtcc 600
cccctggacc cctccaccac ccgctcctcg gtgctcacc tcaccccaca 650
gccccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700
ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctacccgcct 750
cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800
cttgggaaat ggctcatctc tgctactccc agagggccag tctctgcgcc 850
tggctctgtg agttgatgca gttgacagca atccccctgc caggctgagc 900
ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaaccggg 950

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ggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000
 gcagagctca gaacctctc ggctctcagc aggtctacct gaacgtctcc 1050
 ctgcagagca aagccacatc aggagtgact caggggggtgg tcgggggagc 1100
 tggagccaca gccctggtct tcctgtcctt ctgcgtcatc ttcgtttag 1150
 tgaggtcctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat 1200
 acgggcatag aggatgcaaa cgctgtcagg ggttcagcct ctcaggggcc 1250
 cctgactgaa ccttgggcag aagacagtcc ccagaccag cctccccag 1300
 cttctgcccg ctctcagtg ggggaaggag agctccagta tgcattccctc 1350
 agcttcaga tggatgaagc ttgggactcg cggggacagg agggcactga 1400
 caccgagtac tcggagatca agatccacag atgagaaact gcagagactc 1450
 accctgattg agggatcaca gccctccag gcaagggaga agtcagaggc 1500
 tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataaact 1550
 atgaattatg tgcagagtga aaagcacaca ggcttttagag tcaaagtatc 1600
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 acagacaaat tccta 1665

<210> 160

<211> 463

<212> PRT

<213> Homo sapiens

<400> 160

Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala
1				5					10					15
Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr
				20					25					30
Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr
				35					40					45
Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr
				50					55					60
Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala
				65					70					75
Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg
				80					85					90
Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser
				95					100					105
Ile	Arg	Asp	Ala	Arg	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Phe	Phe	Arg

					110					115					120
Met	Glu	Lys	Gly	Ser	Ile	Lys	Trp	Asn	Tyr	Lys	His	His	Arg	Leu	
				125					130					135	
Ser	Val	Asn	Val	Thr	Ala	Leu	Thr	His	Arg	Pro	Asn	Ile	Leu	Ile	
				140					145					150	
Pro	Gly	Thr	Leu	Glu	Ser	Gly	Cys	Pro	Gln	Asn	Leu	Thr	Cys	Ser	
				155					160					165	
Val	Pro	Trp	Ala	Cys	Glu	Gln	Gly	Thr	Pro	Pro	Met	Ile	Ser	Trp	
				170					175					180	
Ile	Gly	Thr	Ser	Val	Ser	Pro	Leu	Asp	Pro	Ser	Thr	Thr	Arg	Ser	
				185					190					195	
Ser	Val	Leu	Thr	Leu	Ile	Pro	Gln	Pro	Gln	Asp	His	Gly	Thr	Ser	
				200					205					210	
Leu	Thr	Cys	Gln	Val	Thr	Phe	Pro	Gly	Ala	Ser	Val	Thr	Thr	Asn	
				215					220					225	
Lys	Thr	Val	His	Leu	Asn	Val	Ser	Tyr	Pro	Pro	Gln	Asn	Leu	Thr	
				230					235					240	
Met	Thr	Val	Phe	Gln	Gly	Asp	Gly	Thr	Val	Ser	Thr	Val	Leu	Gly	
				245					250					255	
Asn	Gly	Ser	Ser	Leu	Ser	Leu	Pro	Glu	Gly	Gln	Ser	Leu	Arg	Leu	
				260					265					270	
Val	Cys	Ala	Val	Asp	Ala	Val	Asp	Ser	Asn	Pro	Pro	Ala	Arg	Leu	
				275					280					285	
Ser	Leu	Ser	Trp	Arg	Gly	Leu	Thr	Leu	Cys	Pro	Ser	Gln	Pro	Ser	
				290					295					300	
Asn	Pro	Gly	Val	Leu	Glu	Leu	Pro	Trp	Val	His	Leu	Arg	Asp	Ala	
				305					310					315	
Ala	Glu	Phe	Thr	Cys	Arg	Ala	Gln	Asn	Pro	Leu	Gly	Ser	Gln	Gln	
				320					325					330	
Val	Tyr	Leu	Asn	Val	Ser	Leu	Gln	Ser	Lys	Ala	Thr	Ser	Gly	Val	
				335					340					345	
Thr	Gln	Gly	Val	Val	Gly	Gly	Ala	Gly	Ala	Thr	Ala	Leu	Val	Phe	
				350					355					360	
Leu	Ser	Phe	Cys	Val	Ile	Phe	Val	Val	Val	Arg	Ser	Cys	Arg	Lys	
				365					370					375	
Lys	Ser	Ala	Arg	Pro	Ala	Ala	Gly	Val	Gly	Asp	Thr	Gly	Ile	Glu	
				380					385					390	
Asp	Ala	Asn	Ala	Val	Arg	Gly	Ser	Ala	Ser	Gln	Gly	Pro	Leu	Thr	
				395					400					405	

Glu	Pro	Trp	Ala	Glu	Asp	Ser	Pro	Pro	Asp	Gln	Pro	Pro	Pro	Ala
				410					415					420
Ser	Ala	Arg	Ser	Ser	Val	Gly	Glu	Gly	Glu	Leu	Gln	Tyr	Ala	Ser
				425					430					435
Leu	Ser	Phe	Gln	Met	Val	Lys	Pro	Trp	Asp	Ser	Arg	Gly	Gln	Glu
				440					445					450
Ala	Thr	Asp	Thr	Glu	Tyr	Ser	Glu	Ile	Lys	Ile	His	Arg		
				455					460					

<210> 161
 <211> 739
 <212> DNA
 <213> Homo sapiens

<400> 161
 gacgcccagt gacctgccga ggtcggcagc acagagctct ggagatgaag 50
 accctgttcc tgggtgtcac gctcggcctg gccgctgccc tgccttcac 100
 cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150
 tcgataagga ctttccggag gacaggaggc ccaggaagggt gtccccagt 200
 aaggtgacag ccctgggcgg tgggaagttg gaagccacgt tcaccttcac 250
 gaggaggat cgggtgcatcc agaagaaaat cctgatgcgg aagacggagg 300
 agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350
 gagctgcccga ggagggacca ctacatcttt tactgcaaag accagcacca 400
 tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450
 accgggaggc cctggaagaa tttaagaaat tgggtgcagcg caagggactc 500
 tcggaggagg acattttcac gcccctgcag acgggaagct gcgttcccga 550
 aactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600
 acacagagcc cggaccacct ggacctacc tccagccatg acccttcct 650
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 162
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 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

20					25					30				
Val	Lys	Ala	Met	Val	Val	Asp	Lys	Asp	Phe	Pro	Glu	Asp	Arg	Arg
			35						40					45
Pro	Arg	Lys	Val	Ser	Pro	Val	Lys	Val	Thr	Ala	Leu	Gly	Gly	Gly
			50						55					60
Lys	Leu	Glu	Ala	Thr	Phe	Thr	Phe	Met	Arg	Glu	Asp	Arg	Cys	Ile
			65						70					75
Gln	Lys	Lys	Ile	Leu	Met	Arg	Lys	Thr	Glu	Glu	Pro	Gly	Lys	Tyr
			80						85					90
Ser	Ala	Tyr	Gly	Gly	Arg	Lys	Leu	Met	Tyr	Leu	Gln	Glu	Leu	Pro
			95						100					105
Arg	Arg	Asp	His	Tyr	Ile	Phe	Tyr	Cys	Lys	Asp	Gln	His	His	Gly
			110						115					120
Gly	Leu	Leu	His	Met	Gly	Lys	Leu	Val	Gly	Arg	Asn	Ser	Asp	Thr
			125						130					135
Asn	Arg	Glu	Ala	Leu	Glu	Glu	Phe	Lys	Lys	Leu	Val	Gln	Arg	Lys
			140						145					150
Gly	Leu	Ser	Glu	Glu	Asp	Ile	Phe	Thr	Pro	Leu	Gln	Thr	Gly	Ser
			155						160					165
Cys	Val	Pro	Glu	His										
			170											

<210> 163
 <211> 22
 <212> DNA
 <213> Artificial
 <220>
 <221> Artificial Sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 163
 ggagatgaag accctgttcc tg 22

<210> 164
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 164
 ggagatgaag accctgttcc tgggtg 26

<210> 165
<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct.

<400> 165
gtcctccgga aagtccttat c 21

<210> 166
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 166
gcctagtgtt cgggaacgca gcttc 25

<210> 167
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 167
cagggacctg gtacgtgaag gccatggtgg tcgataagga ctttccggag 50

<210> 168
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 168
ctgtccttica ccctggagga ggaggatatc acagggacct ggtac 45

<210> 169
<211> 1204
<212> DNA
<213> Homo sapiens

<400> 169

gttccgcaga tgcagaggtt gaggtggctg cgggactgga agtcatcggg 50
cagaggtctc acagcagcca aggaacctgg ggcccgtcc tccccctcc 100
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 150
gtaggggggag agaccaggat catcaagggg ttcgagtgca agcctcactc 200
ccagccctgg caggcagccc tgttcgagaa gacgcggcta ctctgtgggg 250
cgacgctcat cgccccaga tggctcctga cagcagccca ctgcctcaag 300
ccccgctaca tagttcacct ggggcagcac aacctccaga aggaggaggg 350
ctgtgagcag acccggacag ccaactgagtc cttccccac ccgggttca 400
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atggcatcgc cagtctccat cacctgggct gtgcgacccc tcacctctc 500
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attatctcct ggggccagga tccgtgtgcg atcaccgaa agcctggtgt 800
ctacacgaaa gtctgcaa atgtggactg gatccaggag acgatgaaga 850
acaattagac tggaccacc caccacagcc catcaccctc catttccact 900
tggtgtttgg ttctgttca ctctgttaat aagaaaccct aagccaagac 950
cctctacgaa cattctttgg gcctcctgga ctacaggaga tgctgtcact 1000
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aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
aaaa 1204

<210> 170
<211> 250
<212> PRT
<213> Homo sapiens

<400> 170
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His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Phe	Glu	Lys	Thr	Arg	Leu	35	40	45
Leu	Cys	Gly	Ala	Thr	Leu	Ile	Ala	Pro	Arg	Trp	Leu	Leu	Thr	Ala	50	55	60
Ala	His	Cys	Leu	Lys	Pro	Arg	Tyr	Ile	Val	His	Leu	Gly	Gln	His	65	70	75
Asn	Leu	Gln	Lys	Glu	Glu	Gly	Cys	Glu	Gln	Thr	Arg	Thr	Ala	Thr	80	85	90
Glu	Ser	Phe	Pro	His	Pro	Gly	Phe	Asn	Asn	Ser	Leu	Pro	Asn	Lys	95	100	105
Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	Lys	Met	Ala	Ser	Pro	Val	110	115	120
Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	Leu	Ser	Ser	Arg	Cys	125	130	135
Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ser	Thr	140	145	150
Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	Cys	Ala	Asn	155	160	165
Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	Pro	Gly	170	175	180
Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	Gly	185	190	195
Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	200	205	210
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala	215	220	225
Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val	230	235	240
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn						245	250	

<210> 171

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct.

[illegible]

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<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.
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<210> 173
<211> 18
<212> DNA
<213> Artificial
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<400> 173
cctctggtct gtaaccag 18

```
<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.
```

```
<210> 175
<211> 25
<212> DNA
<213> Artificial
```

```
<400> 175
cgtgtagaca ccaggctttc gggtg 25
```

173

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 176

cccttgatga tcctggtc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177

aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178

gagagaccag gatcatcaag gggttcagat gcaagcctca ctc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179

gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50

gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100

aagaaagagg agagcaccga agaagtgaat atagaagttt tgcacgtcc 150

agaaaactgc tctaagacaa gcaagaagg agacctacta aatgccatt 200

atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250

caaaatgaag gccaccccaa atggtttggt cttggtgttg ggcaagtc 300

aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350

aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400

ggcaagattc caccggatgc tacattgatt tttgagattg aactttatgc 450
 tgtgaccaa ggaccacgga gcattgagac atttaaacia atagacatgg 500
 acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550
 gaatttgaaa aagatgagaa gccacgtgac aagtcatatc aggatgcagt 600
 tttagaagat atttttaaga agaatgacca tgatggtgat ggcttcattt 650
 ctccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700
 atttctactt ttttttttta gctatttact gtactttatg tataaaacia 750
 agtcactttt ctccaagttg tatttgctat ttttccccta tgagaagata 800
 ttttgatctc cccaatacat tgattttggg ataataaatg tgaggctgtt 850
 ttgcaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
 aaaaaaa 907

<210> 180
 <211> 222
 <212> PRT
 <213> Homo sapiens

<400> 180
 Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe
 1 5 10 15
 Tyr Leu Trp Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu
 20 25 30
 Ser Thr Glu Glu Val Lys Ile Glu Val Leu His Arg Pro Glu Asn
 35 40 45
 Cys Ser Lys Thr Ser Lys Lys Gly Asp Leu Leu Asn Ala His Tyr
 50 55 60
 Asp Gly Tyr Leu Ala Lys Asp Gly Ser Lys Phe Tyr Cys Ser Arg
 65 70 75
 Thr Gln Asn Glu Gly His Pro Lys Trp Phe Val Leu Gly Val Gly
 80 85 90
 Gln Val Ile Lys Gly Leu Asp Ile Ala Met Thr Asp Met Cys Pro
 95 100 105
 Gly Glu Lys Arg Lys Val Val Ile Pro Pro Ser Phe Ala Tyr Gly
 110 115 120
 Lys Glu Gly Tyr Ala Glu Gly Lys Ile Pro Pro Asp Ala Thr Leu
 125 130 135
 Ile Phe Glu Ile Glu Leu Tyr Ala Val Thr Lys Gly Pro Arg Ser
 140 145 150

Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu
				155					160					165
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys
				170					175					180
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu
				185					190					195
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser
				200					205					210
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu			
				215					220					

<210> 181
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 181
 gtgttctgct ggagccgatg cc 22

<210> 182
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 182
 gacatggaca atgacagg 18

<210> 183
 <211> 18
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-18
 <223> Synthetic construct.

<400> 183
 cctttcagga tgtaggag 18

<210> 184
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 184
 gatgtctgcc accccaag 18

<210> 185
 <211> 27
 <212> DNA
 <213> Artificial

<220>
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 <223> Synthetic construct.

<400> 185
 gcatcctgat atgacttgat acgtggc 27

<210> 186
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 186
 tacaagagg aagaggagt gcac 24

<210> 187
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 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-52
 <223> Synthetic construct.

<400> 187
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 cc 52

<210> 188
 <211> 573
 <212> DNA
 <213> Homo sapiens

<400> 188
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cccaaagtct tctgtgtca ataactca ctgcacctgc aacctggat 150
 atacttctgg atctgggcag aaactattca cattccccctt ggagacatgt 200
 aacgccaggc atggtggctc gcgcctgtaa tcccagttct ttgggaagcc 250
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 ccaaataaag tacttatatt ctc 573

<210> 189

<211> 74

<212> PRT

<213> Homo sapiens

<400> 189

Met	Gln	Gly	Pro	Leu	Leu	Leu	Pro	Gly	Leu	Cys	Phe	Leu	Leu	Ser
1				5					10					15
Leu	Phe	Gly	Ala	Val	Thr	Gln	Lys	Thr	Lys	Thr	Ser	Cys	Ala	Lys
				20					25					30
Cys	Pro	Pro	Asn	Ala	Ser	Cys	Val	Asn	Asn	Thr	His	Cys	Thr	Cys
				35					40					45
Asn	His	Gly	Tyr	Thr	Ser	Gly	Ser	Gly	Gln	Lys	Leu	Phe	Thr	Phe
				50					55					60
Pro	Leu	Glu	Thr	Cys	Asn	Ala	Arg	His	Gly	Gly	Ser	Arg	Leu	
				65					70					

<210> 190

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 190

agggaccatt gcttcttcca ggcc 24

<210> 191

<211> 24

<212> DNA

<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 191
cgttacatgt ctccaagggg aatg 24

<210> 192
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 192
cctgtgctaa gtgccccca aatgcttcct gtgtcaataa cactcactgc 50

<210> 193
<211> 1091
<212> DNA
<213> Homo sapiens

<400> 193
caagcaggtc atccccttgg tgaccttcaa agagaagcag agagggcaga 50
ggtggggggc acagggaaag ggtgacctct gagattcccc ttttccccca 100
gactttggaa gtgaccacc atggggctca gcatcttttt gctcctgtgt 150
gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200
gtgtgggcgt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250
gcctgcgctg cgggggtgtc ottattgacc acaggtgggt cctcacagcg 300
gctcactgca gcggcagcag gtactgggtg cgctggggg aacacagcct 350
cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400
cccatcccgg ctacctggga gcctcgacga gccacgagca cgacctccgg 450
ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccct 500
gcccctgccc aatgactgtg caaccgctgg caccgagtgc cacgtctcag 550
gctggggcat caccaaccac ccacggaacc cattcccga tctgctccag 600
tgctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650
cgggagaatc acgagcaaca tgggtgtgtgc aggcggcgtc ccggggcagg 700
atgcctgcca gggtgattct gggggccccc tgggtgtgtgg gggagtcctt 750
caaggtctgg tgtcctgggg gtctgtgggg ccctgtggac aagatggcat 800

ccctggagtc tacacctata ttgcaagta tgtggactgg atccggatga 850
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 ccctagctcc actcttgttg gcctgggaac ttcttgggaac tttaactcct 1000
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 tggaataaat ataatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194
 <211> 248
 <212> PRT
 <213> Homo sapiens

<400> 194

Met	Gly	Leu	Ser	Ile	Phe	Leu	Leu	Leu	Cys	Val	Leu	Gly	Leu	Ser	1	5	10	15
Gln	Ala	Ala	Thr	Pro	Lys	Ile	Phe	Asn	Gly	Thr	Glu	Cys	Gly	Arg	20	25	30	
Asn	Ser	Gln	Pro	Trp	Gln	Val	Gly	Leu	Phe	Glu	Gly	Thr	Ser	Leu	35	40	45	
Arg	Cys	Gly	Gly	Val	Leu	Ile	Asp	His	Arg	Trp	Val	Leu	Thr	Ala	50	55	60	
Ala	His	Cys	Ser	Gly	Ser	Arg	Tyr	Trp	Val	Arg	Leu	Gly	Glu	His	65	70	75	
Ser	Leu	Ser	Gln	Leu	Asp	Trp	Thr	Glu	Gln	Ile	Arg	His	Ser	Gly	80	85	90	
Phe	Ser	Val	Thr	His	Pro	Gly	Tyr	Leu	Gly	Ala	Ser	Thr	Ser	His	95	100	105	
Glu	His	Asp	Leu	Arg	Leu	Leu	Arg	Leu	Arg	Leu	Pro	Val	Arg	Val	110	115	120	
Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr	125	130	135	
Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His	140	145	150	
Pro	Arg	Asn	Pro	Phe	Pro	Asp	Leu	Leu	Gln	Cys	Leu	Asn	Leu	Ser	155	160	165	
Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile	170	175	180	
Thr	Ser	Asn	Met	Val	Cys	Ala	Gly	Gly	Val	Pro	Gly	Gln	Asp	Ala	185	190	195	
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu				

	200		205		210
Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp					
	215		220		225
Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp					
	230		235		240
Ile Arg Met Ile Met Arg Asn Asn					
	245				

<210> 195
 <211> 1485
 <212> DNA
 <213> Homo sapiens

<400> 195
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 tcgccatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcgttc 150
 ggcttgctca aagcccggca ggagaggagg ctggccgaga tcaaccggga 200
 gtttctgtgt gaccagaagt acagtgatga agagaacctt ccagaaaagc 250
 tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300
 gagattgacc tgatgtcttt aaagaggatg atggagaagc ttggtgtccc 350
 caagaccac ctggagatga agaagatgat ctgagagggt acaggagggg 400
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 gatactgagg ggaccaggat gggagaatga ggagtaaaat gctcacggca 1400
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 tgacccaat ctgcttgaaa aaaaaaaaaa aaaaa 1485

<210> 196
 <211> 150
 <212> PRT
 <213> Homo sapiens

<400> 196
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 Gly Leu Leu Lys Ala Arg Gln Glu Arg Arg Leu Ala Glu Ile Asn
 20 25 30
 Arg Glu Phe Leu Cys Asp Gln Lys Tyr Ser Asp Glu Glu Asn Leu
 35 40 45
 Pro Glu Lys Leu Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp
 50 55 60
 Leu Asn Asn Glu Gly Glu Ile Asp Leu Met Ser Leu Lys Arg Met
 65 70 75
 Met Glu Lys Leu Gly Val Pro Lys Thr His Leu Glu Met Lys Lys
 80 85 90
 Met Ile Ser Glu Val Thr Gly Gly Val Ser Asp Thr Ile Ser Tyr
 95 100 105
 Arg Asp Phe Val Asn Met Met Leu Gly Lys Arg Ser Ala Val Leu
 110 115 120
 Lys Leu Val Met Met Phe Glu Gly Lys Ala Asn Glu Ser Ser Pro
 125 130 135
 Lys Pro Val Gly Pro Pro Pro Glu Arg Asp Ile Ala Ser Leu Pro
 140 145 150

<210> 197
 <211> 4842
 <212> DNA
 <213> Homo sapiens

<400> 197

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ggggtcggcg ccgccgtgcy gcgccgcctg gcgctggcct tggcgctggc 150
gagcgtcctg agtgggcctc cagccgtcgc ctgccccacc aagtgtacct 200
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<210> 198

<211> 1523

<212> PRT

<213> Homo sapiens

<400> 198

Met	Ala	Pro	Gly	Trp	Ala	Gly	Val	Gly	Ala	Ala	Val	Arg	Ala	Arg	1	5	10	15
Leu	Ala	Leu	Ala	Leu	Ala	Leu	Ala	Ser	Val	Leu	Ser	Gly	Pro	Pro	20	25	30	
Ala	Val	Ala	Cys	Pro	Thr	Lys	Cys	Thr	Cys	Ser	Ala	Ala	Ser	Val	35	40	45	
Asp	Cys	His	Gly	Leu	Gly	Leu	Arg	Ala	Val	Pro	Arg	Gly	Ile	Pro	50	55	60	
Arg	Asn	Ala	Glu	Arg	Leu	Asp	Leu	Asp	Arg	Asn	Asn	Ile	Thr	Arg	65	70	75	
Ile	Thr	Lys	Met	Asp	Phe	Ala	Gly	Leu	Lys	Asn	Leu	Arg	Val	Leu	80	85	90	
His	Leu	Glu	Asp	Asn	Gln	Val	Ser	Val	Ile	Glu	Arg	Gly	Ala	Phe	95	100	105	
Gln	Asp	Leu	Lys	Gln	Leu	Glu	Arg	Leu	Arg	Leu	Asn	Lys	Asn	Lys	110	115	120	
Leu	Gln	Val	Leu	Pro	Glu	Leu	Leu	Phe	Gln	Ser	Thr	Pro	Lys	Leu	125	130	135	
Thr	Arg	Leu	Asp	Leu	Ser	Glu	Asn	Gln	Ile	Gln	Gly	Ile	Pro	Arg	140	145	150	
Lys	Ala	Phe	Arg	Gly	Ile	Thr	Asp	Val	Lys	Asn	Leu	Gln	Leu	Asp	155	160	165	

Asn	Asn	His	Ile	Ser	Cys	Ile	Glu	Asp	Gly	Ala	Phe	Arg	Ala	Leu	170	175	180
Arg	Asp	Leu	Glu	Ile	Leu	Thr	Leu	Asn	Asn	Asn	Ile	Ser	Arg		185	190	195
Ile	Leu	Val	Thr	Ser	Phe	Asn	His	Met	Pro	Lys	Ile	Arg	Thr	Leu	200	205	210
Arg	Leu	His	Ser	Asn	His	Leu	Tyr	Cys	Asp	Cys	His	Leu	Ala	Trp	215	220	225
Leu	Ser	Asp	Trp	Leu	Arg	Gln	Arg	Arg	Thr	Val	Gly	Gln	Phe	Thr	230	235	240
Leu	Cys	Met	Ala	Pro	Val	His	Leu	Arg	Gly	Phe	Asn	Val	Ala	Asp	245	250	255
Val	Gln	Lys	Lys	Glu	Tyr	Val	Cys	Pro	Ala	Pro	His	Ser	Glu	Pro	260	265	270
Pro	Ser	Cys	Asn	Ala	Asn	Ser	Ile	Ser	Cys	Pro	Ser	Pro	Cys	Thr	275	280	285
Cys	Ser	Asn	Asn	Ile	Val	Asp	Cys	Arg	Gly	Lys	Gly	Leu	Met	Glu	290	295	300
Ile	Pro	Ala	Asn	Leu	Pro	Glu	Gly	Ile	Val	Glu	Ile	Arg	Leu	Glu	305	310	315
Gln	Asn	Ser	Ile	Lys	Ala	Ile	Pro	Ala	Gly	Ala	Phe	Thr	Gln	Tyr	320	325	330
Lys	Lys	Leu	Lys	Arg	Ile	Asp	Ile	Ser	Lys	Asn	Gln	Ile	Ser	Asp	335	340	345
Ile	Ala	Pro	Asp	Ala	Phe	Gln	Gly	Leu	Lys	Ser	Leu	Thr	Ser	Leu	350	355	360
Val	Leu	Tyr	Gly	Asn	Lys	Ile	Thr	Glu	Ile	Ala	Lys	Gly	Leu	Phe	365	370	375
Asp	Gly	Leu	Val	Ser	Leu	Gln	Leu	Leu	Leu	Leu	Asn	Ala	Asn	Lys	380	385	390
Ile	Asn	Cys	Leu	Arg	Val	Asn	Thr	Phe	Gln	Asp	Leu	Gln	Asn	Leu	395	400	405
Asn	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Lys	Leu	Gln	Thr	Ile	Ser	Lys	410	415	420
Gly	Leu	Phe	Ala	Pro	Leu	Gln	Ser	Ile	Gln	Thr	Leu	His	Leu	Ala	425	430	435
Gln	Asn	Pro	Phe	Val	Cys	Asp	Cys	His	Leu	Lys	Trp	Leu	Ala	Asp	440	445	450
Tyr	Leu	Gln	Asp	Asn	Pro	Ile	Glu	Thr	Ser	Gly	Ala	Arg	Cys	Ser			

	455		460		465
Ser Pro Arg Arg	Leu Ala Asn Lys Arg	Ile Ser Gln Ile Lys Ser			
	470	475			480
Lys Lys Phe Arg	Cys Ser Gly Ser Glu	Asp Tyr Arg Ser Arg Phe			
	485	490			495
Ser Ser Glu Cys	Phe Met Asp Leu Val	Cys Pro Glu Lys Cys Arg			
	500	505			510
Cys Glu Gly Thr	Ile Val Asp Cys Ser	Asn Gln Lys Leu Val Arg			
	515	520			525
Ile Pro Ser His	Leu Pro Glu Tyr Val	Thr Asp Leu Arg Leu Asn			
	530	535			540
Asp Asn Glu Val	Ser Val Leu Glu Ala	Thr Gly Ile Phe Lys Lys			
	545	550			555
Leu Pro Asn Leu	Arg Lys Ile Asn Leu	Ser Asn Asn Lys Ile Lys			
	560	565			570
Glu Val Arg Glu	Gly Ala Phe Asp Gly	Ala Ala Ser Val Gln Glu			
	575	580			585
Leu Met Leu Thr	Gly Asn Gln Leu Glu	Thr Val His Gly Arg Val			
	590	595			600
Phe Arg Gly Leu	Ser Gly Leu Lys Thr	Leu Met Leu Arg Ser Asn			
	605	610			615
Leu Ile Ser Cys	Val Ser Asn Asp Thr	Phe Ala Gly Leu Ser Ser			
	620	625			630
Val Arg Leu Leu	Ser Leu Tyr Asp Asn	Arg Ile Thr Thr Ile Thr			
	635	640			645
Pro Gly Ala Phe	Thr Thr Leu Val Ser	Leu Ser Thr Ile Asn Leu			
	650	655			660
Leu Ser Asn Pro	Phe Asn Cys Asn Cys	His Leu Ala Trp Leu Gly			
	665	670			675
Lys Trp Leu Arg	Lys Arg Arg Ile Val	Ser Gly Asn Pro Arg Cys			
	680	685			690
Gln Lys Pro Phe	Phe Leu Lys Glu Ile	Pro Ile Gln Asp Val Ala			
	695	700			705
Ile Gln Asp Phe	Thr Cys Asp Gly Asn	Glu Glu Ser Ser Cys Gln			
	710	715			720
Leu Ser Pro Arg	Cys Pro Glu Gln Cys	Thr Cys Met Glu Thr Val			
	725	730			735
Val Arg Cys Ser	Asn Lys Gly Leu Arg	Ala Leu Pro Arg Gly Met			
	740	745			750

Pro Lys Asp Val Thr Glu Leu Tyr Leu Glu Gly Asn His Leu Thr	755	760	765
Ala Val Pro Arg Glu Leu Ser Ala Leu Arg His Leu Thr Leu Ile	770	775	780
Asp Leu Ser Asn Asn Ser Ile Ser Met Leu Thr Asn Tyr Thr Phe	785	790	795
Ser Asn Met Ser His Leu Ser Thr Leu Ile Leu Ser Tyr Asn Arg	800	805	810
Leu Arg Cys Ile Pro Val His Ala Phe Asn Gly Leu Arg Ser Leu	815	820	825
Arg Val Leu Thr Leu His Gly Asn Asp Ile Ser Ser Val Pro Glu	830	835	840
Gly Ser Phe Asn Asp Leu Thr Ser Leu Ser His Leu Ala Leu Gly	845	850	855
Thr Asn Pro Leu His Cys Asp Cys Ser Leu Arg Trp Leu Ser Glu	860	865	870
Trp Val Lys Ala Gly Tyr Lys Glu Pro Gly Ile Ala Arg Cys Ser	875	880	885
Ser Pro Glu Pro Met Ala Asp Arg Leu Leu Leu Thr Thr Pro Thr	890	895	900
His Arg Phe Gln Cys Lys Gly Pro Val Asp Ile Asn Ile Val Ala	905	910	915
Lys Cys Asn Ala Cys Leu Ser Ser Pro Cys Lys Asn Asn Gly Thr	920	925	930
Cys Thr Gln Asp Pro Val Glu Leu Tyr Arg Cys Ala Cys Pro Tyr	935	940	945
Ser Tyr Lys Gly Lys Asp Cys Thr Val Pro Ile Asn Thr Cys Ile	950	955	960
Gln Asn Pro Cys Gln His Gly Gly Thr Cys His Leu Ser Asp Ser	965	970	975
His Lys Asp Gly Phe Ser Cys Ser Cys Pro Leu Gly Phe Glu Gly	980	985	990
Gln Arg Cys Glu Ile Asn Pro Asp Asp Cys Glu Asp Asn Asp Cys	995	1000	1005
Glu Asn Asn Ala Thr Cys Val Asp Gly Ile Asn Asn Tyr Val Cys	1010	1015	1020
Ile Cys Pro Pro Asn Tyr Thr Gly Glu Leu Cys Asp Glu Val Ile	1025	1030	1035
Asp His Cys Val Pro Glu Leu Asn Leu Cys Gln His Glu Ala Lys			

1040	1045	1050
Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly		
1055	1060	1065
Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala		
1070	1075	1080
His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly		
1085	1090	1095
Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu		
1100	1105	1110
His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln		
1115	1120	1125
Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu		
1130	1135	1140
Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu		
1145	1150	1155
Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu		
1160	1165	1170
Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln		
1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp		
1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu		
1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val		
1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr		
1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys		
1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser		
1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala		
1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys		
1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala		
1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys		
1325	1330	1335

Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser
1340 1345 1350

Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp
1355 1360 1365

Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly
1370 1375 1380

Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu
1385 1390 1395

Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn
1400 1405 1410

Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser
1415 1420 1425

Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly
1430 1435 1440

Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg
1445 1450 1455

Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala
1460 1465 1470

Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln
1475 1480 1485

Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln
1490 1495 1500

Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu
1505 1510 1515

Glu Cys Gly Cys Leu Ala Cys Ser
1520

<210> 199
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 199
atggagattc ctgccaaactt gccg 24

<210> 200
<211> 24
<212> DNA
<213> Artificial

<220>

<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 200
ttgttggcat tgaggaggag cagc 24

<210> 201
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 201
gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202
<211> 753
<212> DNA
<213> Homo sapiens

<400> 202
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gtttcttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100
gaatctgcct tttcagttct gtctccggca ggctttgagg atgaaggctg 150
cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200
atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250
caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300
agagcggcta caacaccaca gccccgacgg tcctggatga cggcagcatc 350
gactatggca tcttcagat caacagcttc gcgtggtgca gacgcggaaa 400
gctgaaggag aacaaccact gccatgtgc ctgctcagcc ttgatcactg 450
atgacctcac agatgcaatt atctgtgccg ggaaaattgt taaagagaca 500
caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550
cctgtccgag tggaaaaaag gctgtgaggt ttcttaaact ggaactggac 600
ccaggatgct ttgcagcaac gccctaggat ttgcagtga tgtccaaatg 650
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gagggaaaat taagctatac ttttaagaaa ataaatattt ccatttaa 750
gtc 753

<210> 203
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 203
 Met Lys Ala Ala Gly Ile Leu Thr Leu Ile Gly Cys Leu Val Thr
 1 5 10 15
 Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile
 20 25 30
 Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly
 35 40 45
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr
 50 55 60
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe
 65 70 75
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu
 80 85 90
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp
 95 100 105
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr
 110 115 120
 Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly
 125 130 135
 Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
 140 145

<210> 204
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 204
 gcaggctttg aggatgaagg ctgc 24

<210> 205
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 205
ctcattggct gcctggtcac aggc 24

<210> 206
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 206
ccagtcggac aggtctctcc cctc 24

<210> 207
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 207
tcagtgacca aggctgagca ggcg 24

<210> 208
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 208
ctacactcgt tgcaaactgg caaaaatatt ctcgagggt ggcctgg 47

<210> 209
<211> 1648
<212> DNA
<213> Homo sapiens

<400> 209
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ctttttacct tggTgtctgc ctgtatccca gtgttcaggc tggctagacg 200
gcggaagaag atcctatTTT actgtcactt cccagatctg cttctcacca 250

agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300
 gaggaatata ccacaggcat ggcagactgc atcttagtca acagccagtt 350
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 cctgaaaagc tggatgacct agtccccaag gggaaaaaat tcctgctgct 500
 ctccatcaac agatacgaaa ggaagaaaaa tctgactttg gcaactggaag 550
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 tgtccctctg gaagccatgt acatgcagtg ccagtcatt gctgttaatt 850
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 tcaactgtcat ctgttaggga atttttgttt gtctgtctt tgcctggatc 1550
 catagcgaga gtgctctgta ttttttttaa gataatttgt atttttgcac 1600
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<210> 210
 <211> 323

<212> PRT

<213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly	
1				5					10					15	
Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val	
				20					25					30	
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His	
				35					40					45	
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg	
				50					55					60	
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly	
				65					70					75	
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val	
				80					85					90	
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val	
				95					100					105	
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro	
				110					115					120	
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu	
				125					130					135	
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala	
				140					145					150	
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp	
				155					160					165	
Trp	Glu	Arg	Val	His	Leu	Ile	Val	Ala	Gly	Gly	Tyr	Asp	Glu	Arg	
				170					175					180	
Val	Leu	Glu	Asn	Val	Glu	His	Tyr	Gln	Glu	Leu	Lys	Lys	Met	Val	
				185					190					195	
Gln	Gln	Ser	Asp	Leu	Gly	Gln	Tyr	Val	Thr	Phe	Leu	Arg	Ser	Phe	
				200					205					210	
Ser	Asp	Lys	Gln	Lys	Ile	Ser	Leu	Leu	His	Ser	Cys	Thr	Cys	Val	
				215					220					225	
Leu	Tyr	Thr	Pro	Ser	Asn	Glu	His	Phe	Gly	Ile	Val	Pro	Leu	Glu	
				230					235					240	
Ala	Met	Tyr	Met	Gln	Cys	Pro	Val	Ile	Ala	Val	Asn	Ser	Gly	Gly	
				245					250					255	
Pro	Leu	Glu	Ser	Ile	Asp	His	Ser	Val	Thr	Gly	Phe	Leu	Cys	Glu	
				260					265					270	

Pro	Asp	Pro	Val	His	Phe	Ser	Glu	Ala	Ile	Glu	Lys	Phe	Ile	Arg
				275					280					285
Glu	Pro	Ser	Leu	Lys	Ala	Thr	Met	Gly	Leu	Ala	Gly	Arg	Ala	Arg
				290					295					300
Val	Lys	Glu	Lys	Phe	Ser	Pro	Glu	Ala	Phe	Thr	Glu	Gln	Leu	Tyr
				305					310					315
Arg	Tyr	Val	Thr	Lys	Leu	Leu	Val							
				320										

<210> 211

<211> 1554

<212> DNA

<213> Homo sapiens

<400> 211

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ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtgaag 200
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gttttgctat gaagtctgtt acacagatgg taatgggtag tacatttgaa 600
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tgactcctta gtacaagga accctaatga ccaacagatc ctagaagaca 850
gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900
tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950
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 cattgttaaa ttgattgagg aaaacaacca tttaaaaaaa atctatgttg 1500
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 ttaa 1554

<210> 212

<211> 462

<212> PRT

<213> Homo sapiens

<400> 212

Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu
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Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala
 20 25 30

Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu
 35 40 45

Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn
 50 55 60

Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg
 65 70 75

Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His
 80 85 90

Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys
 95 100 105

Ser Leu Leu Arg Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn
 110 115 120

His Met Arg Lys Lys Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu
 125 130 135

Lys Ser Asn Phe Ala Leu Leu Leu Lys Leu Ser Glu Glu Leu Leu

				140					145					150
Asp	Lys	Trp	Leu	Ser 155	Tyr	Pro	Glu	Thr	Gln 160	His	Val	Pro	Leu	Ser 165
Gln	His	Met	Leu	Gly 170	Phe	Ala	Met	Lys	Ser 175	Val	Thr	Gln	Met	Val 180
Met	Gly	Ser	Thr	Phe 185	Glu	Asp	Asp	Gln	Glu 190	Val	Ile	Arg	Phe	Gln 195
Lys	Asn	His	Gly	Thr 200	Val	Trp	Ser	Glu	Ile 205	Gly	Lys	Gly	Phe	Leu 210
Asp	Gly	Ser	Leu	Asp 215	Lys	Asn	Met	Thr	Arg 220	Lys	Lys	Gln	Tyr	Glu 225
Asp	Ala	Leu	Met	Gln 230	Leu	Glu	Ser	Val	Leu 235	Arg	Asn	Ile	Ile	Lys 240
Glu	Arg	Lys	Gly	Arg 245	Asn	Phe	Ser	Gln	His 250	Ile	Phe	Ile	Asp	Ser 255
Leu	Val	Gln	Gly	Asn 260	Leu	Asn	Asp	Gln	Gln 265	Ile	Leu	Glu	Asp	Ser 270
Met	Ile	Phe	Ser	Leu 275	Ala	Ser	Cys	Ile	Ile 280	Thr	Ala	Lys	Leu	Cys 285
Thr	Trp	Ala	Ile	Cys 290	Phe	Leu	Thr	Thr	Ser 295	Glu	Glu	Val	Gln	Lys 300
Lys	Leu	Tyr	Glu	Glu 305	Ile	Asn	Gln	Val	Phe 310	Gly	Asn	Gly	Pro	Val 315
Thr	Pro	Glu	Lys	Ile 320	Glu	Gln	Leu	Arg	Tyr 325	Cys	Gln	His	Val	Leu 330
Cys	Glu	Thr	Val	Arg 335	Thr	Ala	Lys	Leu	Thr 340	Pro	Val	Ser	Ala	Gln 345
Leu	Gln	Asp	Ile	Glu 350	Gly	Lys	Ile	Asp	Arg 355	Phe	Ile	Ile	Pro	Arg 360
Glu	Thr	Leu	Val	Leu 365	Tyr	Ala	Leu	Gly	Val 370	Val	Leu	Gln	Asp	Pro 375
Asn	Thr	Trp	Pro	Ser 380	Pro	His	Lys	Phe	Asp 385	Pro	Asp	Arg	Phe	Asp 390
Asp	Glu	Leu	Val	Met 395	Lys	Thr	Phe	Ser	Ser 400	Leu	Gly	Phe	Ser	Gly 405
Thr	Gln	Glu	Cys	Pro 410	Glu	Leu	Arg	Phe	Ala 415	Tyr	Met	Val	Thr	Thr 420
Val	Leu	Leu	Ser	Val 425	Leu	Val	Lys	Arg	Leu 430	His	Leu	Leu	Ser	Val 435

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser
 440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr
 455 460

<210> 213
 <211> 759
 <212> DNA
 <213> Homo sapiens

<400> 213
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 tcagggcttg tgccctctcg ctctctgacg ctcttgccgc atctgggtgg 150
 cgtcatcacc ttattctggg cccgggacag caacatacag gcctgcctgc 200
 ctctcaggtt ccccccgag gagtatgaca agcaggacat tcagctgggtg 250
 gccgcgctct ctgtcacctt gggcctcttt gcagtggagc tggccgggtt 300
 cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350
 gggctcactg tagtgcaccc gtggccctgt ccttcttcat attcgagcgt 400
 tgggagtgca ctacgtattg gtacattttt gtcttctgca gtgcccttcc 450
 agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500
 aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550
 ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcgggt 600
 ttcccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650
 tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700
 tgtttttag tagtaattaag acttatatac agtttttagg gacaattaaa 750
 aaaaaaaaa 759

<210> 214
 <211> 140
 <212> PRT
 <213> Homo sapiens

<400> 214
 Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu
 1 5 10 15
 Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp
 20 25 30
 Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
 35 40 45

Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr
50 55 60
Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val
65 70 75
Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His
80 85 90
Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp
95 100 105
Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu
110 115 120
Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu
125 130 135
Lys Lys Lys Pro Phe
140

<210> 215
<211> 697
<212> DNA
<213> Homo sapiens

<400> 215
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gaccggcct gctgcagccc catagtgcc cggaacgagt ggaaggccct 150
ggcatcagag tgcgccagc acctgagcct gccottacgc tatgtggtgg 200
tatcgcacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250
caggcccgga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300
cgtgggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350
gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400
tccattggca tcagcttcat gggcaactac atggatcggg tgcccacacc 450
ccaggccatc cgggcagccc aggggtctact ggctgcgggt gtggctcagg 500
gagccctgag gtccaactat gtgctcaaag gacaccggga tgtgcagcgt 550
aactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600
ctaccgctcc ccctgaggcc ctgctgatcc gcacccatt cctccctcc 650
catggccaaa aacccactg tctccttctc caataaagat gtagctc 697

<210> 216
<211> 196
<212> PRT

<213> Homo sapiens

<400> 216

Met Ser Arg Arg Ser Met Leu Leu Ala Trp Ala Leu Pro Ser Leu
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Leu Arg Leu Gly Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys
20 25 30
Ser Pro Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu
35 40 45
Cys Ala Gln His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser
50 55 60
His Thr Ala Gly Ser Ser Cys Asn Thr Pro Ala Ser Cys Gln Gln
65 70 75
Gln Ala Arg Asn Val Gln His Tyr His Met Lys Thr Leu Gly Trp
80 85 90
Cys Asp Val Gly Tyr Asn Phe Leu Ile Gly Glu Asp Gly Leu Val
95 100 105
Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly Ala His Ser Gly His
110 115 120
Leu Trp Asn Pro Met Ser Ile Gly Ile Ser Phe Met Gly Asn Tyr
125 130 135
Met Asp Arg Val Pro Thr Pro Gln Ala Ile Arg Ala Ala Gln Gly
140 145 150
Leu Leu Ala Cys Gly Val Ala Gln Gly Ala Leu Arg Ser Asn Tyr
155 160 165
Val Leu Lys Gly His Arg Asp Val Gln Arg Thr Leu Ser Pro Gly
170 175 180
Asn Gln Leu Tyr His Leu Ile Gln Asn Trp Pro His Tyr Arg Ser
185 190 195
Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

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tctatctggt catctgtggc caggatgatg gtcctcccgg ctgagaggac 150
cctgagcgtg atgaccacga gggccagccc cggccccggg tgcctcgga 200

gogggggccac atctcaccta agtcccggccc catggccaat tccactctcc 250
tagggctgct gggcccgccct ggggaggctt ggggcattct tgggcagccc 300
cccaaccgcc cgaaccacag cccccacccc tcagccaagg tgaagaaaat 350
ctttggctgg ggcgacttct actccaacat caagacggtg gccctgaacc 400
tgctcgtcac aggggaagatt gtggaccatg gcaatgggac cttcagcgtc 450
catttccaac acaatgccac aggccaggga aacatctcca tcagcctcgt 500
ggcccccagt aaagctgtag agttccacca ggaacagcag atcttcatcg 550
aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta 600
gaacgggggc gccggacctc gctttgcacc cacgacccag ccaagatctg 650
ctcccgagac cacgctcaga gctcagccac ctggagctgc tccagccct 700
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gtccagaagg tgtgccaga ttacaactac catagtata cccctacta 800
cccatctggg tgaccggggg caggccacag aggcaggcc agggctggaa 850
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gttgggcctc aggcaggag gggggtggag acgaggagat gccaagtggg 950
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tgttctgtgt gtctgtctgt ggggtggggg aggggagggg agtcttgtga 1800
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aataaagctt gccccgggc a 1871

<210> 218
<211> 252
<212> PRT
<213> Homo sapiens

<400> 218
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Leu Tyr Leu Val Ile Cys Gly Gln Asp Asp Gly Pro Pro Gly Ser
20 25 30
Glu Asp Pro Glu Arg Asp Asp His Glu Gly Gln Pro Arg Pro Arg
35 40 45
Val Pro Arg Lys Arg Gly His Ile Ser Pro Lys Ser Arg Pro Met
50 55 60
Ala Asn Ser Thr Leu Leu Gly Leu Leu Ala Pro Pro Gly Glu Ala
65 70 75
Trp Gly Ile Leu Gly Gln Pro Pro Asn Arg Pro Asn His Ser Pro
80 85 90
Pro Pro Ser Ala Lys Val Lys Lys Ile Phe Gly Trp Gly Asp Phe
95 100 105
Tyr Ser Asn Ile Lys Thr Val Ala Leu Asn Leu Leu Val Thr Gly
110 115 120
Lys Ile Val Asp His Gly Asn Gly Thr Phe Ser Val His Phe Gln
125 130 135
His Asn Ala Thr Gly Gln Gly Asn Ile Ser Ile Ser Leu Val Pro
140 145 150
Pro Ser Lys Ala Val Glu Phe His Gln Glu Gln Gln Ile Phe Ile
155 160 165
Glu Ala Lys Ala Ser Lys Ile Phe Asn Cys Arg Met Glu Trp Glu
170 175 180
Lys Val Glu Arg Gly Arg Arg Thr Ser Leu Cys Thr His Asp Pro
185 190 195
Ala Lys Ile Cys Ser Arg Asp His Ala Gln Ser Ser Ala Thr Trp
200 205 210

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe
215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr
230 235 240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly
245 250

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

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gggttctgca tgagctcctt aaaggacaaa ggtaacagag ccagcgagag 150
agctcgaggg gagactttga cttcaagcca cagaattggg ggaagtgtgc 200
gcgcgcgcgc cgccgtcgct cctgcagcgc tgtcgacctg gccgctagca 250
tcttcccgag caccgggatc ccggggtagg aggcgacgcg ggcgagcacc 300
agcgccagcc ggctgcggct gccacacggt ctcaccatgg gctccgggcg 350
ccgggcgctg tccgcggtgc cggccgtgct gctggctctc acgctgccgg 400
ggctgcccgt ctgggcacag aacgacacgg agcccatcgt gctggagggc 450
aagtgtctgg tgggtgtgca ctgcaaccgg gccacggact ccaagggctc 500
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ccttctcggc ggtgcggagc accaaccacg agccatccga gatgagcaac 600
aagacgcgca tcatttactt cgatcagatc ctggtgaatg tgggtaattt 650
tttcacattg gagtctgtct ttgtagcacc aagaaaagga atttacagtt 700
tcagttttca cgtgattaaa gtctaccaga gccaaactat ccaggttaac 750
ttgatgttaa atggaaaacc agtaatatct gcctttgcgg gggacaaaaga 800
tgttactcgt gaagctgccg cgaatgggtg cctgctctac ctagataaaag 850
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cagtattcca cgttttctgg ctttctggtg ttccccctat aggattcaat 950
ttctccatga tgttcatcca ggtgagggat gaccactcc tgagttattg 1000
gaagatcatt ttttcatcat tggattgatg tcttttattg gtttctcatg 1050
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tcacagatta tttgtgtgtg tctgtttcag tatatttgga ttgggactct 1150
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ttataacctat ttttcaaggc ttctgttgta ttgaagtat catctggttt 1900
tgcttaact ctttaaattg tatatattta tctgttttagc taatattaa 1950
ttcaaataat ccatatctaa atttagtga atatcttgct tttgtatag 2000
gtcatatgaa ttcataaaat tatttatgct tgttatagaa taaagattaa 2050
tatatgttaa aaaaa 2065

<210> 220
<211> 201
<212> PRT
<213> Homo sapiens

<400> 220
Met Gly Ser Gly Arg Arg Ala Leu Ser Ala Val Pro Ala Val Leu
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Leu Val Leu Thr Leu Pro Gly Leu Pro Val Trp Ala Gln Asn Asp
20 25 30
Thr Glu Pro Ile Val Leu Glu Gly Lys Cys Leu Val Val Cys Asp
35 40 45
Ser Asn Pro Ala Thr Asp Ser Lys Gly Ser Ser Ser Ser Pro Leu
50 55 60

Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala	
				65					70					75	
Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr	
				80					85					90	
Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe	
				95					100					105	
Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr	
				110					115					120	
Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile	
				125					130					135	
Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe	
				140					145					150	
Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val	
				155					160					165	
Leu	Leu	Tyr	Leu	Asp	Lys	Glu	Asp	Lys	Val	Tyr	Leu	Lys	Leu	Glu	
				170					175					180	
Lys	Gly	Asn	Leu	Val	Gly	Gly	Trp	Gln	Tyr	Ser	Thr	Phe	Ser	Gly	
				185					190					195	
Phe	Leu	Val	Phe	Pro	Leu										
				200											

<210> 221
 <211> 20
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

 <400> 221
 acggctcacc atgggctccg 20

 <210> 222
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 222
 aggaagagga gcccttggag tccg 24

 <210> 223
 <211> 40

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-40
<223> Synthetic construct.

<400> 223
cgtgctggag ggcaagtgtc tgggtggtgtg cgactcgaac 40

<210> 224
<211> 902
<212> DNA
<213> Homo sapiens

<400> 224
cgggtggccat gactgcggcc gtgttcttcg gctgcgcctt cattgccttc 50
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tatcatcttc ctcatcgccg gagctttctt ctggttggtg tctctactga 150
tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200
ggaccaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta 250
tatccaagaa atgttccgat ttgcatatta taaactctta aaaaaagcca 300
gtgaaggttt gaagagtata aaccacaggtg agacagcacc ctctatgcga 350
ctgctggcct atgtttctgg cttgggcttt ggaatcatga gtggagtatt 400
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ttcatggaga ttctcctcaa ttcttccttt attcagcttt catgacgctg 500
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tgaaaatccc tttttctggt ggaattgaga aagaaataaa actatgcaga 900
ta 902

<210> 225
<211> 257
<212> PRT

<213> Homo sapiens

<400> 225

Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile Ala Phe Gly
1 5 10 15

Pro Ala Leu Ala Leu Tyr Val Phe Thr Ile Ala Ile Glu Pro Leu
20 25 30

Arg Ile Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val Ser
35 40 45

Leu Leu Ile Ser Ser Leu Val Trp Phe Met Ala Arg Val Ile Ile
50 55 60

Asp Asn Lys Asp Gly Pro Thr Gln Lys Tyr Leu Leu Ile Phe Gly
65 70 75

Ala Phe Val Ser Val Tyr Ile Gln Glu Met Phe Arg Phe Ala Tyr
80 85 90

Tyr Lys Leu Leu Lys Lys Ala Ser Glu Gly Leu Lys Ser Ile Asn
95 100 105

Pro Gly Glu Thr Ala Pro Ser Met Arg Leu Leu Ala Tyr Val Ser
110 115 120

Gly Leu Gly Phe Gly Ile Met Ser Gly Val Phe Ser Phe Val Asn
125 130 135

Thr Leu Ser Asp Ser Leu Gly Pro Gly Thr Val Gly Ile His Gly
140 145 150

Asp Ser Pro Gln Phe Phe Leu Tyr Ser Ala Phe Met Thr Leu Val
155 160 165

Ile Ile Leu Leu His Val Phe Trp Gly Ile Val Phe Phe Asp Gly
170 175 180

Cys Glu Lys Lys Lys Trp Gly Ile Leu Leu Ile Val Leu Leu Thr
185 190 195

His Leu Leu Val Ser Ala Gln Thr Phe Ile Ser Ser Tyr Tyr Gly
200 205 210

Ile Asn Leu Ala Ser Ala Phe Ile Ile Leu Val Leu Met Gly Thr
215 220 225

Trp Ala Phe Leu Ala Ala Gly Gly Ser Cys Arg Ser Leu Lys Leu
230 235 240

Cys Leu Leu Cys Gln Asp Lys Asn Phe Leu Leu Tyr Asn Gln Arg
245 250 255

Ser Arg

<210> 226

<211> 3939
<212> DNA
<213> Homo sapiens

<400> 226

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agtttgagcg cacctacgtg gacgaggtca acagcgagct ggtcaacatc 200
tacaccttca accatactgt gacccgcaac aggacagagg gcgtgcgtgt 250
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gttaccaggg ccgctccttt gaacctgtag gtactcggcc ccgagtggac 1250
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 aacaacatcc tcagcaacct ggggtacatc ctgctggggc tgcttttct 1600
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 gacatcaacg ccagcgccca cagtgcctac gcctgcctgg ccattgtcat 1900
 ctctctctct gtgctggggc tggcttttg caaagggaac acggcgcttct 1950
 ggatcgtctt ctccatcatt cacatcatcg ccacctgct cctcagcacg 2000
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 tgcacggtt gcacctccgt ggtctggggc ttgcgctct tcttcttctt 2350
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<210> 227

<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

Met	Phe	Ala	Leu	Gly	Leu	Pro	Phe	Leu	Val	Leu	Leu	Val	Ala	Ser
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Val	Glu	Ser	His	Leu	Gly	Val	Leu	Gly	Pro	Lys	Asn	Val	Ser	Gln
				20					25					30

	320		325		330
Ile Asp Arg Ala	Cys Pro Glu Ser Gly	His Pro Arg Val Leu	Ala		
	335	340	345		
Asp Ser Phe Pro	Gly Ser Ser Pro Tyr	Glu Gly Tyr Asn Tyr	Gly		
	350	355	360		
Ser Phe Glu Asn	Val Ser Gly Ser Thr	Asp Gly Leu Val Asp	Ser		
	365	370	375		
Ala Gly Thr Gly	Asp Leu Ser Tyr Gly	Tyr Gln Gly Arg Ser	Phe		
	380	385	390		
Glu Pro Val Gly	Thr Arg Pro Arg Val	Asp Ser Met Ser Ser	Val		
	395	400	405		
Glu Glu Asp Asp	Tyr Asp Thr Leu Thr	Asp Ile Asp Ser Asp	Lys		
	410	415	420		
Asn Val Ile Arg	Thr Lys Gln Tyr Leu	Tyr Val Ala Asp Leu	Ala		
	425	430	435		
Arg Lys Asp Lys	Arg Val Leu Arg Lys	Lys Tyr Gln Ile Tyr	Phe		
	440	445	450		
Trp Asn Ile Ala	Thr Ile Ala Val Phe	Tyr Ala Leu Pro Val	Val		
	455	460	465		
Gln Leu Val Ile	Thr Tyr Gln Thr Val	Val Asn Val Thr Gly	Asn		
	470	475	480		
Gln Asp Ile Cys	Tyr Tyr Asn Phe Leu	Cys Ala His Pro Leu	Gly		
	485	490	495		
Asn Leu Ser Ala	Phe Asn Asn Ile Leu	Ser Asn Leu Gly Tyr	Ile		
	500	505	510		
Leu Leu Gly Leu	Leu Phe Leu Leu Ile	Ile Leu Gln Arg Glu	Ile		
	515	520	525		
Asn His Asn Arg	Ala Leu Leu Arg Asn	Asp Leu Cys Ala Leu	Glu		
	530	535	540		
Cys Gly Ile Pro	Lys His Phe Gly Leu	Phe Tyr Ala Met Gly	Thr		
	545	550	555		
Ala Leu Met Met	Glu Gly Leu Leu Ser	Ala Cys Tyr His Val	Cys		
	560	565	570		
Pro Asn Tyr Thr	Asn Phe Gln Phe Asp	Thr Ser Phe Met Tyr	Met		
	575	580	585		
Ile Ala Gly Leu	Cys Met Leu Lys Leu	Tyr Gln Lys Arg His	Pro		
	590	595	600		
Asp Ile Asn Ala	Ser Ala Tyr Ser Ala	Tyr Ala Cys Leu Ala	Ile		
	605	610	615		

Val	Ile	Phe	Phe	Ser	Val	Leu	Gly	Val	Val	Phe	Gly	Lys	Gly	Asn	
				620					625					630	
Thr	Ala	Phe	Trp	Ile	Val	Phe	Ser	Ile	Ile	His	Ile	Ile	Ala	Thr	
				635					640					645	
Leu	Leu	Leu	Ser	Thr	Gln	Leu	Tyr	Tyr	Met	Gly	Arg	Trp	Lys	Leu	
				650					655					660	
Asp	Ser	Gly	Ile	Phe	Arg	Arg	Ile	Leu	His	Val	Leu	Tyr	Thr	Asp	
				665					670					675	
Cys	Ile	Arg	Gln	Cys	Ser	Gly	Pro	Leu	Tyr	Val	Asp	Arg	Met	Val	
				680					685					690	
Leu	Leu	Val	Met	Gly	Asn	Val	Ile	Asn	Trp	Ser	Leu	Ala	Ala	Tyr	
				695					700					705	
Gly	Leu	Ile	Met	Arg	Pro	Asn	Asp	Phe	Ala	Ser	Tyr	Leu	Leu	Ala	
				710					715					720	
Ile	Gly	Ile	Cys	Asn	Leu	Leu	Leu	Tyr	Phe	Ala	Phe	Tyr	Ile	Ile	
				725					730					735	
Met	Lys	Leu	Arg	Ser	Gly	Glu	Arg	Ile	Lys	Leu	Ile	Pro	Leu	Leu	
				740					745					750	
Cys	Ile	Val	Cys	Thr	Ser	Val	Val	Trp	Gly	Phe	Ala	Leu	Phe	Phe	
				755					760					765	
Phe	Phe	Gln	Gly	Leu	Ser	Thr	Trp	Gln	Lys	Thr	Pro	Ala	Glu	Ser	
				770					775					780	
Arg	Glu	His	Asn	Arg	Asp	Cys	Ile	Leu	Leu	Asp	Phe	Phe	Asp	Asp	
				785					790					795	
His	Asp	Ile	Trp	His	Phe	Leu	Ser	Ser	Ile	Ala	Met	Phe	Gly	Ser	
				800					805					810	
Phe	Leu	Val	Leu	Leu	Thr	Leu	Asp	Asp	Asp	Leu	Asp	Thr	Val	Gln	
				815					820					825	
Arg	Asp	Lys	Ile	Tyr	Val	Phe									
				830											

<210> 228

<211> 2848

<212> DNA

<213> Homo sapiens

<400> 228

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ttgggcgctg gagggcctgt cctgaccatg gtccctgcct ggctgtggct 150

gctttgtgtc tccgtccccc aggctctccc caaggcccag cctgcagagc 200

tgtctgtgga agttccagaa aactatggtg gaaatttccc tttatacctg 250
 accaagttgc cgctgccccg tgagggggct gaaggccaga tcgtgctgtc 300
 aggggactca ggcaaggcaa ctgaggggcc atttgctatg gatccagatt 350
 ctggcttctt gctggtgacc agggccctgg accgagagga gcaggcagag 400
 taccagctac aggtcacctt ggagatgcag gatggacatg tcttgtgggg 450
 tccacagcct gtgcttgtgc acgtgaagga tgagaatgac caggtgcccc 500
 atttctctca agccatctac agagctcggc tgagccgggg taccaggcct 550
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<210> 229

<211> 807

<212> PRT

<213> Homo sapiens

<400> 229

Met	Val	Pro	Ala	Trp	Leu	Trp	Leu	Leu	Cys	Val	Ser	Val	Pro	Gln
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Ala Leu Pro Lys Ala Gln Pro Ala Glu Leu Ser Val Glu Val Pro

	20		25		30
Glu Asn Tyr Gly	Gly Asn Phe Pro Leu Tyr	Leu Thr Lys Leu Pro			
	35		40		45
Leu Pro Arg Glu	Gly Ala Glu Gly Gln Ile Val Leu Ser Gly Asp				
	50		55		60
Ser Gly Lys Ala Thr	Glu Gly Pro Phe Ala Met Asp Pro Asp Ser				
	65		70		75
Gly Phe Leu Leu Val	Thr Arg Ala Leu Asp Arg Glu Glu Gln Ala				
	80		85		90
Glu Tyr Gln Leu Gln	Val Thr Leu Glu Met Gln Asp Gly His Val				
	95		100		105
Leu Trp Gly Pro Gln	Pro Val Leu Val His Val Lys Asp Glu Asn				
	110		115		120
Asp Gln Val Pro His	Phe Ser Gln Ala Ile Tyr Arg Ala Arg Leu				
	125		130		135
Ser Arg Gly Thr Arg	Pro Gly Ile Pro Phe Leu Phe Leu Glu Ala				
	140		145		150
Ser Asp Arg Asp Glu	Pro Gly Thr Ala Asn Ser Asp Leu Arg Phe				
	155		160		165
His Ile Leu Ser Gln	Ala Pro Ala Gln Pro Ser Pro Asp Met Phe				
	170		175		180
Gln Leu Glu Pro Arg	Leu Gly Ala Leu Ala Leu Ser Pro Lys Gly				
	185		190		195
Ser Thr Ser Leu Asp	His Ala Leu Glu Arg Thr Tyr Gln Leu Leu				
	200		205		210
Val Gln Val Lys Asp	Met Gly Asp Gln Ala Ser Gly His Gln Ala				
	215		220		225
Thr Ala Thr Val Glu	Val Ser Ile Ile Glu Ser Thr Trp Val Ser				
	230		235		240
Leu Glu Pro Ile His	Leu Ala Glu Asn Leu Lys Val Leu Tyr Pro				
	245		250		255
His His Met Ala Gln	Val His Trp Ser Gly Gly Asp Val His Tyr				
	260		265		270
His Leu Glu Ser His	Pro Pro Gly Pro Phe Glu Val Asn Ala Glu				
	275		280		285
Gly Asn Leu Tyr Val	Thr Arg Glu Leu Asp Arg Glu Ala Gln Ala				
	290		295		300
Glu Tyr Leu Leu Gln	Val Arg Ala Gln Asn Ser His Gly Glu Asp				
	305		310		315

Tyr Ala Ala Pro	Leu Glu Leu His Val	Leu Val Met Asp Glu Asn	320	325	330
Asp Asn Val Pro	Ile Cys Pro Pro Arg	Asp Pro Thr Val Ser Ile	335	340	345
Pro Glu Leu Ser	Pro Pro Gly Thr Glu	Val Thr Arg Leu Ser Ala	350	355	360
Glu Asp Ala Asp	Ala Pro Gly Ser Pro	Asn Ser His Val Val Tyr	365	370	375
Gln Leu Leu Ser	Pro Glu Pro Glu Asp	Gly Val Glu Gly Arg Ala	380	385	390
Phe Gln Val Asp	Pro Thr Ser Gly Ser	Val Thr Leu Gly Val Leu	395	400	405
Pro Leu Arg Ala	Gly Gln Asn Ile Leu	Leu Leu Val Leu Ala Met	410	415	420
Asp Leu Ala Gly	Ala Glu Gly Gly Phe	Ser Ser Thr Cys Glu Val	425	430	435
Glu Val Ala Val	Thr Asp Ile Asn Asp	His Ala Pro Glu Phe Ile	440	445	450
Thr Ser Gln Ile	Gly Pro Ile Ser Leu	Pro Glu Asp Val Glu Pro	455	460	465
Gly Thr Leu Val	Ala Met Leu Thr Ala	Ile Asp Ala Asp Leu Glu	470	475	480
Pro Ala Phe Arg	Leu Met Asp Phe Ala	Ile Glu Arg Gly Asp Thr	485	490	495
Glu Gly Thr Phe	Gly Leu Asp Trp Glu	Pro Asp Ser Gly His Val	500	505	510
Arg Leu Arg Leu	Cys Lys Asn Leu Ser	Tyr Glu Ala Ala Pro Ser	515	520	525
His Glu Val Val	Val Val Val Gln Ser	Val Ala Lys Leu Val Gly	530	535	540
Pro Gly Pro Gly	Pro Gly Ala Thr Ala	Thr Val Thr Val Leu Val	545	550	555
Glu Arg Val Met	Pro Pro Pro Lys Leu	Asp Gln Glu Ser Tyr Glu	560	565	570
Ala Ser Val Pro	Ile Ser Ala Pro Ala	Gly Ser Phe Leu Leu Thr	575	580	585
Ile Gln Pro Ser	Asp Pro Ile Ser Arg	Thr Leu Arg Phe Ser Leu	590	595	600
Val Asn Asp Ser	Glu Gly Trp Leu Cys	Ile Glu Lys Phe Ser Gly			

605	610	615
Glu Val His Thr	Ala Gln Ser Leu Gln	Gly Ala Gln Pro Gly Asp
620	625	630
Thr Tyr Thr Val	Leu Val Glu Ala Gln	Asp Thr Ala Leu Thr Leu
635	640	645
Ala Pro Val Pro	Ser Gln Tyr Leu Cys	Thr Pro Arg Gln Asp His
650	655	660
Gly Leu Ile Val	Ser Gly Pro Ser Lys	Asp Pro Asp Leu Ala Ser
665	670	675
Gly His Gly Pro	Tyr Ser Phe Thr Leu	Gly Pro Asn Pro Thr Val
680	685	690
Gln Arg Asp Trp	Arg Leu Gln Thr Leu	Asn Gly Ser His Ala Tyr
695	700	705
Leu Thr Leu Ala	Leu His Trp Val Glu	Pro Arg Glu His Ile Ile
710	715	720
Pro Val Val Val	Ser His Asn Ala Gln	Met Trp Gln Leu Leu Val
725	730	735
Arg Val Ile Val	Cys Arg Cys Asn Val	Glu Gly Gln Cys Met Arg
740	745	750
Lys Val Gly Arg	Met Lys Gly Met Pro	Thr Lys Leu Ser Ala Val
755	760	765
Gly Ile Leu Val	Gly Thr Leu Val Ala	Ile Gly Ile Phe Leu Ile
770	775	780
Leu Ile Phe Thr	His Trp Thr Met Ser	Arg Lys Lys Asp Pro Asp
785	790	795
Gln Pro Ala Asp	Ser Val Pro Leu Lys	Ala Thr Val
800	805	

<210> 230
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 230
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<210> 231
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> Artificial Sequence
 <222> full
 <223> Synthetic oligonucleotide probe

<400> 231
 cctgagctgt aaccccactc cagg 24

<210> 232
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 232
 agagtctgtc ccagctatct tgt 23

<210> 233
 <211> 2786
 <212> DNA
 <213> Homo sapiens

<400> 233
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 atctgtggcc aagaaaaatt ttttggggac caagttttga ggattaatgt 100
 cagaaatgga gacgagatca gcaaattgag tcaactagtg aattcaaaca 150
 acttgaagct caatttctgg aaatctccct cctccttcaa tcggcctgtg 200
 gatgtcctgg tcccatctgt cagtctgcag gcattttaa ccttcctgag 250
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 tagacaatga agatgatgaa atgcaacaca atgaagggca agaacggagc 350
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 agattggaca ttcgtttgaa aaccggccga tgtatgtact gaagttcagc 500
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 ccaataaata ttcaatgtga aaaaaaaaaa aaaaaa 2786

<210> 234

<211> 421

<212> PRT

<213> Homo sapiens

<400> 234

Met	Arg	Trp	Ile	Leu	Phe	Ile	Gly	Ala	Leu	Ile	Gly	Ser	Ser	Ile
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Cys	Gly	Gln	Glu	Lys	Phe	Phe	Gly	Asp	Gln	Val	Leu	Arg	Ile	Asn
				20					25					30
Val	Arg	Asn	Gly	Asp	Glu	Ile	Ser	Lys	Leu	Ser	Gln	Leu	Val	Asn
				35					40					45
Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe
				50					55					60
Asn	Arg	Pro	Val	Asp	Val	Leu	Val	Pro	Ser	Val	Ser	Leu	Gln	Ala
				65					70					75
Phe	Lys	Ser	Phe	Leu	Arg	Ser	Gln	Gly	Leu	Glu	Tyr	Ala	Val	Thr
				80					85					90
Ile	Glu	Asp	Leu	Gln	Ala	Leu	Leu	Asp	Asn	Glu	Asp	Asp	Glu	Met
				95					100					105
Gln	His	Asn	Glu	Gly	Gln	Glu	Arg	Ser	Ser	Asn	Asn	Phe	Asn	Tyr
				110					115					120
Gly	Ala	Tyr	His	Ser	Leu	Glu	Ala	Ile	Tyr	His	Glu	Met	Asp	Asn
				125					130					135
Ile	Ala	Ala	Asp	Phe	Pro	Asp	Leu	Ala	Arg	Arg	Val	Lys	Ile	Gly
				140					145					150
His	Ser	Phe	Glu	Asn	Arg	Pro	Met	Tyr	Val	Leu	Lys	Phe	Ser	Thr
				155					160					165

Gly Lys Gly Val	Arg Arg Pro Ala Val	Trp Leu Asn Ala Gly Ile	170	175	180
His Ser Arg Glu	Trp Ile Ser Gln Ala	Thr Ala Ile Trp Thr Ala	185	190	195
Arg Lys Ile Val	Ser Asp Tyr Gln Arg	Asp Pro Ala Ile Thr Ser	200	205	210
Ile Leu Glu Lys	Met Asp Ile Phe Leu	Leu Pro Val Ala Asn Pro	215	220	225
Asp Gly Tyr Val	Tyr Thr Gln Thr Gln	Asn Arg Leu Trp Arg Lys	230	235	240
Thr Arg Ser Arg	Asn Pro Gly Ser Ser	Cys Ile Gly Ala Asp Pro	245	250	255
Asn Arg Asn Trp	Asn Ala Ser Phe Ala	Gly Lys Gly Ala Ser Asp	260	265	270
Asn Pro Cys Ser	Glu Val Tyr His Gly	Pro His Ala Asn Ser Glu	275	280	285
Val Glu Val Lys	Ser Val Val Asp Phe	Ile Gln Lys His Gly Asn	290	295	300
Phe Lys Gly Phe	Ile Asp Leu His Ser	Tyr Ser Gln Leu Leu Met	305	310	315
Tyr Pro Tyr Gly	Tyr Ser Val Lys Lys	Ala Pro Asp Ala Glu Glu	320	325	330
Leu Asp Lys Val	Ala Arg Leu Ala Ala	Lys Ala Leu Ala Ser Val	335	340	345
Ser Gly Thr Glu	Tyr Gln Val Gly Pro	Thr Cys Thr Thr Val Tyr	350	355	360
Pro Ala Ser Gly	Ser Ser Ile Asp Trp	Ala Tyr Asp Asn Gly Ile	365	370	375
Lys Phe Ala Phe	Thr Phe Glu Leu Arg	Asp Thr Gly Thr Tyr Gly	380	385	390
Phe Leu Leu Pro	Ala Asn Gln Ile Ile	Pro Thr Ala Glu Glu Thr	395	400	405
Trp Leu Gly Leu	Lys Thr Ile Met Glu	His Val Arg Asp Asn Leu	410	415	420

Tyr

<210> 235
 <211> 1743
 <212> DNA
 <213> Homo sapiens

<400> 235

caaccatgca aggacagggc aggagaagag gaacctgcaa agacatattt 50
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ctgtgctcca atctactgtg tgtccccggc caatgcccc agtgcatacc 150
cccgcccttc ctccacaaag agcaccctg cctcacaggt gtattccctc 200
aacaccgact ttgccttccg cctataccgc aggctggttt tggagacccc 250
gagtcagaac atcttcttct cccctgtgag tgtctccact tccctggcca 300
tgctctccct tggggccac tcagtcacca agaccagat tctccagggc 350
ctgggcttca acctcacaca cacaccagag tctgccatcc accagggctt 400
ccagcacctg gttcactcac tgactgttc cagcaaagac ctgacctga 450
agatgggaag tgccctcttc gtcaagaagg agctgcagct gcaggcaa 500
ttcttgggca atgtcaagag gctgtatgaa gcagaagtct tttctacaga 550
tttctccaac cctccattg cccaggcgag gatcaacagc catgtgaaaa 600
agaagacca agggaagggt gtagacataa tccaaggcct tgaccttctg 650
acggccatgg ttctggtgaa tcacattttc tttaaagcca agtgggagaa 700
gccctttcac cttgaatata caagaaagaa cttccattc ctggtgggcg 750
agcaggtcac tgtgcaagtc cccatgatgc accagaaaga gcagttcgct 800
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aactggaaca ggccttgtca gccagaacac tgataaagtg gagccactca 950
ctccagaaaa ggtggataga ggtgttcac cccagatttt ccatttctgc 1000
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gtccccttta cttcactgtc tccttcaata ggaccttcct gatgatgatt 1250
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cactaaatcc taggtgggaa atggcctgtt aactgatggc acattgctaa 1350
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tgaccccagt ggagctggat tcgctggcag ggatgccact tccaaggctc 1450

aatcaccaaa ccatcaacag ggacccagc cacaagccaa caccattaa 1500
 cccagtcag tgcccttttc cacaaattct cccaggtaac tagcttcatg 1550
 ggatgttgct gggttacat atttccattc cttggggctc ccaggaatgg 1600
 aaatacgcca acccaggtta ggcacctcta ttgcagaatt acaataaacac 1650
 attcaataaa actaaaatat gaattcaaaa aaaaaaaaaa aaaaaaaaaa 1700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

<210> 236
 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 236
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 Ala Pro Ile Tyr Cys Val Ser Pro Ala Asn Ala Pro Ser Ala Tyr
 20 25 30
 Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr
 35 40 45
 Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val
 50 55 60
 Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val
 65 70 75
 Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr
 80 85 90
 Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr
 95 100 105
 Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser
 110 115 120
 Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala
 125 130 135
 Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly
 140 145 150
 Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe
 155 160 165
 Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys
 170 175 180
 Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp
 185 190 195
 Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala

Lys Trp Glu Lys	Pro Phe His Leu Glu	Tyr Thr Arg Lys Asn Phe
	215	220 225
Pro Phe Leu Val	Gly Glu Gln Val Thr	Val Gln Val Pro Met Met
	230	235 240
His Gln Lys Glu	Gln Phe Ala Phe Gly	Val Asp Thr Glu Leu Asn
	245	250 255
Cys Phe Val Leu	Gln Met Asp Tyr Lys	Gly Asp Ala Val Ala Phe
	260	265 270
Phe Val Leu Pro	Ser Lys Gly Lys Met	Arg Gln Leu Glu Gln Ala
	275	280 285
Leu Ser Ala Arg	Thr Leu Ile Lys Trp	Ser His Ser Leu Gln Lys
	290	295 300
Arg Trp Ile Glu	Val Phe Ile Pro Arg	Phe Ser Ile Ser Ala Ser
	305	310 315
Tyr Asn Leu Glu	Thr Ile Leu Pro Lys	Met Gly Ile Gln Asn Ala
	320	325 330
Phe Asp Lys Asn	Ala Asp Phe Ser Gly	Ile Ala Lys Arg Asp Ser
	335	340 345
Leu Gln Val Ser	Lys Ala Thr His Lys	Ala Val Leu Asp Val Ser
	350	355 360
Glu Glu Gly Thr	Glu Ala Thr Ala Ala	Thr Thr Thr Lys Phe Ile
	365	370 375
Val Arg Ser Lys	Asp Gly Pro Ser Tyr	Phe Thr Val Ser Phe Asn
	380	385 390
Arg Thr Phe Leu	Met Met Ile Thr Asn	Lys Ala Thr Asp Gly Ile
	395	400 405
Leu Phe Leu Gly	Lys Val Glu Asn Pro	Thr Lys Ser
	410	415

- <210> 237
- <211> 23
- <212> DNA
- <213> Artificial
- <220>
- <221> Artificial Sequence
- <222> 1-23
- <223> Synthetic construct.
- <400> 237
- caaccatgca aggacagggc agg 23
- <210> 238

<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 238
ctttgctgtt ggcctctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 239
tgactcgggg tctccaaaac cagg 24

<210> 240
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 240
ggtataggcg gaaggcaaag tcgg 24

<210> 241
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 241
ggcatcttac ctttatggag tactctttgc tgttggcctc tgtgctcc 48

<210> 242
<211> 2436
<212> DNA
<213> Homo sapiens

<400> 242
ggctgaccgt gctacattgc ctggaggaag cctaaggaac ccaggcatcc 50

agctgcccac gcctgagtcc aagattcttc ccaggaacac aaacgtagga 100
gacccacgct cctggaagca ccagccttta tctcttcacc ttcaagtccc 150
ctttctcaag aatcctctgt tctttgccct ctaaagtctt ggtacatcta 200
ggacccagge atcttgcttt ccagccacaa agagacagat gaagatgcag 250
aaaggaaatg ttctccttat gtttggtcta ctattgcatt tagaagctgc 300
aacaaattcc aatgagacta gcacctctgc caaacttga tccagtgtga 350
tctccagtgg agccagcaca gccaccaact ctgggtccag tgtgacctcc 400
agtgggggtca gcacagccac catctcaggg tccagcgtga cctccaatgg 450
ggtcagcata gtcaccaact ctgagttcca tacaacctcc agtgggatca 500
gcacagccac caactctgag ttcagcacag cgtccagtgg gatcagcata 550
gccaccaact ctgagtccag cacaacctcc agtggggcca gcacagccac 600
caactctgag tccagcacac cctccagtgg ggccagcaca gtcaccaact 650
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cacaacctcc agtggggccg gcacagccac caactctgag tccagcacag 1250
tgtccagtgg gatcagcaca gtcaccaatt ctgagtccag cacacctcc 1300
agtggggcca acacagccac caactctgag tccagtacga cctccagtgg 1350
ggccaacaca gccaccaact ctgagtccag cacagtgtcc agtggggcca 1400
gcactgccac caactctgag tccagcacia cctccagtgg ggtcagcaca 1450
gccaccaact ctgagtccag cacaacctcc agtggggcta gcacagccac 1500

Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala	
				80					85					90	
Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala	
				95					100					105	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				110					115					120	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Ser	Thr	Val	
				125					130					135	
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				140					145					150	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	
				155					160					165	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Leu	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				170					175					180	
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				185					190					195	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				200					205					210	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	
				215					220					225	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				230					235					240	
Thr	Asn	Ser	Glu	Ser	Arg	Thr	Thr	Ser	Asn	Gly	Ala	Gly	Thr	Ala	
				245					250					255	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				260					265					270	
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				275					280					285	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				290					295					300	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				305					310					315	
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Gly	Thr	Ala	
				320					325					330	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val	
				335					340					345	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Asn	Thr	Ala	
				350					355					360	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala	

	365		370		375
Thr Asn Ser Glu	Ser Ser Thr Val Ser	Ser Ser Gly Ala Ser Thr	Ala		
	380		385		390
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Ser Gly Val Ser Thr	Ala		
	395		400		405
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Ser Gly Ala Ser Thr	Ala		
	410		415		420
Thr Asn Ser Asp	Ser Ser Thr Thr Ser	Ser Ser Glu Ala Ser Thr	Ala		
	425		430		435
Thr Asn Ser Glu	Ser Ser Thr Val Ser	Ser Ser Gly Ile Ser Thr	Val		
	440		445		450
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Ser Gly Ala Asn Thr	Ala		
	455		460		465
Thr Asn Ser Gly	Ser Ser Val Thr Ser	Ala Gly Ser Gly Thr	Ala		
	470		475		480
Ala Leu Thr Gly	Met His Thr Thr Ser	His Ser Ala Ser Thr	Ala		
	485		490		495
Val Ser Glu Ala	Lys Pro Gly Gly Ser	Leu Val Pro Trp Glu	Ile		
	500		505		510
Phe Leu Ile Thr	Leu Val Ser Val Val	Ala Ala Val Gly Leu	Phe		
	515		520		525
Ala Gly Leu Phe	Phe Cys Val Arg Asn	Ser Leu Ser Leu Arg	Asn		
	530		535		540
Thr Phe Asn Thr	Ala Val Tyr His Pro	His Gly Leu Asn His	Gly		
	545		550		555
Leu Gly Pro Gly	Pro Gly Gly Asn His	Gly Ala Pro His Arg	Pro		
	560		565		570
Arg Trp Ser Pro	Asn Trp Phe Trp Arg	Arg Pro Val Ser Ser	Ile		
	575		580		585
Ala Met Glu Met	Ser Gly Arg Asn Ser	Gly Pro			
	590		595		

<210> 244

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic sequence.

<400> 245

gtcagagttg gtggctgtgc tagc 24

<210> 246

<211> 48

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-48

<223> Synthetic construct.

<400> 246

ggaccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247

<211> 957

<212> DNA

<213> Homo sapiens

<400> 247

gggagagagg ataaatagca gcgtggcttc cctggctcct ctctgcatcc 50

ttcccgacct tcccagcaat atgcatcttg cacgtctggt cggctcctgc 100

tccctccttc tgctactggg ggccctgtct ggatgggagg ccagcgatga 150

ccccattgag aaggtcattg aagggatcaa ccgagggctg agcaatgcag 200

agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250

gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300

ccacaccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350

tggacaaggt tgcccatgag atcaaccatg gtattggaca agcaggaaaag 400

gaagcagaga agcttggcca tggggtcaac aacgctgctg gacaggccgg 450

gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtccaccagg 500

ctgggaagga agcagagaaa cttggccaag ggggtcaacca tgctgctgac 550

caggctggaa aggaagtgga gaagcttggc caaggtgccc accatgctgc 600

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 ccagcaagga ggccaaccag ctgctgaatg gcaaccatca aagcggatct 700
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 gttgtcacat cagctgacat gacctggagg ggttgggggt gggggacagg 900
 tttctgaaat ccctgaaggg ggttgtactg ggatttgtga ataaacttga 950
 tacacca 957

<210> 248

<211> 247

<212> PRT

<213> Homo sapiens

<400> 248

Met	His	Leu	Ala	Arg	Leu	Val	Gly	Ser	Cys	Ser	Leu	Leu	Leu	Leu	1	5	10	15
Leu	Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu	20	25	30	
Lys	Val	Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg	35	40	45	
Glu	Val	Gly	Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His	50	55	60	
Ala	Gly	Arg	Glu	Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met	65	70	75	
Gly	Ser	His	Thr	Gly	Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu	80	85	90	
Asn	His	Gly	Met	Asp	Lys	Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile	95	100	105	
Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	Asn	110	115	120	
Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln	125	130	135	
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	140	145	150	
Leu	Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu	155	160	165	
Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala	170	175	180	

Gly	Lys	Glu	Leu	Gln	Asn	Ala	His	Asn	Gly	Val	Asn	Gln	Ala	Ser
				185					190					195
Lys	Glu	Ala	Asn	Gln	Leu	Leu	Asn	Gly	Asn	His	Gln	Ser	Gly	Ser
				200					205					210
Ser	Ser	His	Gln	Gly	Gly	Ala	Thr	Thr	Thr	Pro	Leu	Ala	Ser	Gly
				215					220					225
Ala	Ser	Val	Asn	Thr	Pro	Phe	Ile	Asn	Leu	Pro	Ala	Leu	Trp	Arg
				230					235					240
Ser	Val	Ala	Asn	Ile	Met	Pro								
				245										

<210> 249
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 249
 caatatgcat cttgcacgtc tgg 23

<210> 250
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 250
 aagcttctct gcttcctttc ctgc 24

<210> 251
 <211> 43
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-43
 <223> Synthetic construct.

<400> 251
 tgacccatt gagaaggatca ttgaaggat caaccgaggg ctg 43

<210> 252
 <211> 3781
 <212> DNA
 <213> Homo sapiens

<400> 252

ctccgggtcc ccaggggctg cgccgggccg gcctggcaag ggggacgagt 50
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tgaccctgac tactccagg tccggaggcg ggggcccccg gggcgactcg 150
ggggcggacc gcggggcgga gctgccgccc gtgagtccgg ccgagccacc 200
tgagcccgag ccgcgggaca ccgtcgctcc tgctctccga atgtctgcga 250
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gacgagaagg ggaatgtcct cctggaagat ggcaagggcc gttgtccctt 800
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caaagccttc gccccaccaa gaccgagagc tccctcaact ggctgcaaga 950
cccagctttt gtggcctcag cctacattcc tgagagcctg ggcagcttgc 1000
aaggcgatga tgacaagatc tactttttct tcagcgagac tggccaggaa 1050
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gggcgatgag ggtggagagc ggggtgctaca gcagcgtgg acctccttcc 1150
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gtgctgcagg atgtcttcac gctgagcccc agccccagg actggcgtga 1250
cacccttttc tatggggtct tcacttccca gtggcacagg ggaactacag 1300
aaggctctgc cgtctgtgtc ttcacaatga aggatgtgca gagagtcttc 1350
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gaccaccccg gtgcccacac cccggcctgg agcgtgcatc accaacagtg 1450

cccgggaaag gaagatcaac tcatccctgc agctoccaga ccgcgtgctg 1500
 aacttcctca aggaccactt cctgatggac gggcaggtcc gaagccgcat 1550
 gctgctgctg cagccccagg ctcgctacca gcgcgtggct gtacaccgcg 1600
 tccctggcct gcaccacacc tacgatgtcc tcttcctggg cactggtgac 1650
 ggccgggctcc acaaggcagt gagcgtgggc ccccggtgc acatcattga 1700
 ggagctgcag atctttctcat cgggacagcc cgtgcagaat ctgctcctgg 1750
 acaccacag ggggctgctg tatgcggcct cacactcggg cgtagtccag 1800
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 cgcccgggac ccctactgtg cttggagcgg ctccagctgc aagcacgtca 1900
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<211> 837

<212> PRT

<213> Homo sapiens

<400> 253

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Trp	Gly	Ala	Leu	Pro	Pro	Arg	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu
				20					25					30
Leu	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Pro	Pro	Thr	Trp	Ala	Leu	Ser
				35					40					45
Pro	Arg	Ile	Ser	Leu	Pro	Leu	Gly	Ser	Glu	Glu	Arg	Pro	Phe	Leu
				50					55					60
Arg	Phe	Glu	Ala	Glu	His	Ile	Ser	Asn	Tyr	Thr	Ala	Leu	Leu	Leu
				65					70					75
Ser	Arg	Asp	Gly	Arg	Thr	Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Leu

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Phe	Ala	Leu	Ser	Ser	Asn	Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr					
				95					100					105					
Gln	Glu	Leu	Leu	Trp	Gly	Ala	Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys					
				110					115					120					
Ser	Phe	Lys	Gly	Lys	Asp	Pro	Gln	Arg	Asp	Cys	Gln	Asn	Tyr	Ile					
				125					130					135					
Lys	Ile	Leu	Leu	Pro	Leu	Ser	Gly	Ser	His	Leu	Phe	Thr	Cys	Gly					
				140					145					150					
Thr	Ala	Ala	Phe	Ser	Pro	Met	Cys	Thr	Tyr	Ile	Asn	Met	Glu	Asn					
				155					160					165					
Phe	Thr	Leu	Ala	Arg	Asp	Glu	Lys	Gly	Asn	Val	Leu	Leu	Glu	Asp					
				170					175					180					
Gly	Lys	Gly	Arg	Cys	Pro	Phe	Asp	Pro	Asn	Phe	Lys	Ser	Thr	Ala					
				185					190					195					
Leu	Val	Val	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Thr	Val	Ser	Ser	Phe					
				200					205					210					
Gln	Gly	Asn	Asp	Pro	Ala	Ile	Ser	Arg	Ser	Gln	Ser	Leu	Arg	Pro					
				215					220					225					
Thr	Lys	Thr	Glu	Ser	Ser	Leu	Asn	Trp	Leu	Gln	Asp	Pro	Ala	Phe					
				230					235					240					
Val	Ala	Ser	Ala	Tyr	Ile	Pro	Glu	Ser	Leu	Gly	Ser	Leu	Gln	Gly					
				245					250					255					
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Ser	Glu	Thr	Gly	Gln	Glu					
				260					265					270					
Phe	Glu	Phe	Phe	Glu	Asn	Thr	Ile	Val	Ser	Arg	Ile	Ala	Arg	Ile					
				275					280					285					
Cys	Lys	Gly	Asp	Glu	Gly	Gly	Glu	Arg	Val	Leu	Gln	Gln	Arg	Trp					
				290					295					300					
Thr	Ser	Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Ser	Arg	Pro	Asp	Asp					
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Gly	Phe	Pro	Phe	Asn	Val	Leu	Gln	Asp	Val	Phe	Thr	Leu	Ser	Pro					
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Ser	Pro	Gln	Asp	Trp	Arg	Asp	Thr	Leu	Phe	Tyr	Gly	Val	Phe	Thr					
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Ser	Gln	Trp	His	Arg	Gly	Thr	Thr	Glu	Gly	Ser	Ala	Val	Cys	Val					
				350					355					360					
Phe	Thr	Met	Lys	Asp	Val	Gln	Arg	Val	Phe	Ser	Gly	Leu	Tyr	Lys					
				365					370					375					

Glu Val Asn Arg	Glu Thr Gln Gln Trp	Tyr Thr Val Thr His Pro	380	385	390
Val Pro Thr Pro	Arg Pro Gly Ala Cys	Ile Thr Asn Ser Ala Arg	395	400	405
Glu Arg Lys Ile	Asn Ser Ser Leu Gln	Leu Pro Asp Arg Val Leu	410	415	420
Asn Phe Leu Lys	Asp His Phe Leu Met	Asp Gly Gln Val Arg Ser	425	430	435
Arg Met Leu Leu	Leu Gln Pro Gln Ala	Arg Tyr Gln Arg Val Ala	440	445	450
Val His Arg Val	Pro Gly Leu His His	Thr Tyr Asp Val Leu Phe	455	460	465
Leu Gly Thr Gly	Asp Gly Arg Leu His	Lys Ala Val Ser Val Gly	470	475	480
Pro Arg Val His	Ile Ile Glu Glu Leu	Gln Ile Phe Ser Ser Gly	485	490	495
Gln Pro Val Gln	Asn Leu Leu Leu Asp	Thr His Arg Gly Leu Leu	500	505	510
Tyr Ala Ala Ser	His Ser Gly Val Val	Gln Val Pro Met Ala Asn	515	520	525
Cys Ser Leu Tyr	Arg Ser Cys Gly Asp	Cys Leu Leu Ala Arg Asp	530	535	540
Pro Tyr Cys Ala	Trp Ser Gly Ser Ser	Cys Lys His Val Ser Leu	545	550	555
Tyr Gln Pro Gln	Leu Ala Thr Arg Pro	Trp Ile Gln Asp Ile Glu	560	565	570
Gly Ala Ser Ala	Lys Asp Leu Cys Ser	Ala Ser Ser Val Val Ser	575	580	585
Pro Ser Phe Val	Pro Thr Gly Glu Lys	Pro Cys Glu Gln Val Gln	590	595	600
Phe Gln Pro Asn	Thr Val Asn Thr Leu	Ala Cys Pro Leu Leu Ser	605	610	615
Asn Leu Ala Thr	Arg Leu Trp Leu Arg	Asn Gly Ala Pro Val Asn	620	625	630
Ala Ser Ala Ser	Cys His Val Leu Pro	Thr Gly Asp Leu Leu Leu	635	640	645
Val Gly Thr Gln	Gln Leu Gly Glu Phe	Gln Cys Trp Ser Leu Glu	650	655	660
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<400> 256
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<210> 257
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<212> DNA
<213> Artificial

<220>
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<223> Synthetic construct.

<400> 257
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<210> 258
<211> 45
<212> DNA
<213> Artificial

<220>
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<222> 1-45
<223> Synthetic construct.

<400> 258
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<210> 259
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<212> DNA
<213> Homo sapiens

<220>
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<223> unknown base

<400> 259
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<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

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Ala Ser Glu Leu Lys Arg Ala Gly Pro Arg Arg Arg Ala Ser Pro
35 40 45

Glu Gly Cys Arg Ser Gly Gln Ala Ala Ala Ser Gln Ala Gly Gly
50 55 60

Ala Arg Gly Asp Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser
65 70 75

Asp Pro Asp Gly Gly Pro Arg Asp Arg Asn Phe Leu Phe Val Gly
80 85 90

Val Met Thr Ala Gln Lys Tyr Leu Gln Thr Arg Ala Val Ala Ala
95 100 105

Tyr Arg Thr Trp Ser Lys Thr Ile Pro Gly Lys Val Gln Phe Phe
110 115 120

Ser Ser Glu Gly Ser Asp Thr Ser Val Pro Ile Pro Val Val Pro
125 130 135

Leu Arg Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe
140 145 150

Met Met Leu Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu
155 160 165

Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Arg
170 175 180

Leu Glu Asn Phe Leu Arg Ser Leu Asn Ser Ser Glu Pro Leu Phe
185 190 195

Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly Lys Leu
200 205 210

Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Val
215 220 225

Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly
230 235 240

Lys	Cys	Leu	Arg	Glu	Met	Tyr	Thr	Thr	His	Glu	Asp	Val	Glu	Val	
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Gly	Arg	Cys	Val	Arg	Arg	Phe	Ala	Gly	Val	Gln	Cys	Val	Trp	Ser	
				260					265					270	
Tyr	Glu	Met	Arg	Gln	Leu	Phe	Tyr	Glu	Asn	Tyr	Glu	Gln	Asn	Lys	
				275					280					285	
Lys	Gly	Tyr	Ile	Arg	Asp	Leu	His	Asn	Ser	Lys	Ile	His	Gln	Ala	
				290					295					300	
Ile	Thr	Leu	His	Pro	Asn	Lys	Asn	Pro	Pro	Tyr	Gln	Tyr	Arg	Leu	
				305					310					315	
His	Ser	Tyr	Met	Leu	Ser	Arg	Lys	Ile	Ser	Glu	Leu	Arg	His	Arg	
				320					325					330	
Thr	Ile	Gln	Leu	His	Arg	Glu	Ile	Val	Leu	Met	Ser	Lys	Tyr	Ser	
				335					340					345	
Asn	Thr	Glu	Ile	His	Lys	Glu	Asp	Leu	Gln	Leu	Gly	Ile	Pro	Pro	
				350					355					360	
Ser	Phe	Met	Arg	Phe	Gln	Pro	Arg	Gln	Arg	Glu	Glu	Ile	Leu	Glu	
				365					370					375	
Trp	Glu	Phe	Leu	Thr	Gly	Lys	Tyr	Leu	Tyr	Ser	Ala	Val	Asp	Gly	
				380					385					390	
Gln	Pro	Pro	Arg	Arg	Gly	Met	Asp	Ser	Ala	Gln	Arg	Glu	Ala	Leu	
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Asp	Asp	Ile	Val	Met	Gln	Val	Met	Glu	Met	Ile	Asn	Ala	Asn	Ala	
				410					415					420	
Lys	Thr	Arg	Gly	Arg	Ile	Ile	Asp	Phe	Lys	Glu	Ile	Gln	Tyr	Gly	
				425					430					435	
Tyr	Arg	Arg	Val	Asn	Pro	Met	Tyr	Gly	Ala	Glu	Tyr	Ile	Leu	Asp	
				440					445					450	
Leu	Leu	Leu	Leu	Tyr	Lys	Lys	His	Lys	Gly	Lys	Lys	Met	Thr	Val	
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Pro	Val	Arg	Arg	His	Ala	Tyr	Leu	Gln	Gln	Thr	Phe	Ser	Lys	Ile	
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Gln	Phe	Val	Glu	His	Glu	Glu	Leu	Asp	Ala	Gln	Glu	Leu	Ala	Lys	
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Leu	Lys	Lys	Leu	Val	Pro	Phe	Gln	Leu	Pro	Gly	Ser	Lys	Ser	Glu	
				515					520					525	
His	Lys	Glu	Pro	Lys	Asp	Lys	Lys	Ile	Asn	Ile	Leu	Ile	Pro	Leu	

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Lys Thr Cys Leu Ile Pro Asn Gln Asn	Val Lys Leu Val Val	Leu
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Leu Phe Asn Ser Asp Ser Asn Pro Asp	Lys Ala Lys Gln Val	Glu
575	580	585
Leu Met Arg Asp Tyr Arg Ile Lys Tyr	Pro Lys Ala Asp Met	Gln
590	595	600
Ile Leu Pro Val Ser Gly Glu Phe Ser	Arg Ala Leu Ala Leu	Glu
605	610	615
Val Gly Ser Ser Gln Phe Asn Asn Glu	Ser Leu Leu Phe Phe	Cys
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Asp Val Asp Leu Val Phe Thr Thr Glu	Phe Leu Gln Arg Cys	Arg
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Ala Asn Thr Val Leu Gly Gln Gln Ile	Tyr Phe Pro Ile Ile	Phe
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Ser Gln Tyr Asp Pro Lys Ile Val Tyr	Ser Gly Lys Val Pro	Ser
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Asp Asn His Phe Ala Phe Thr Gln Lys	Thr Gly Phe Trp Arg	Asn
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Tyr Gly Phe Gly Ile Thr Cys Ile Tyr	Lys Gly Asp Leu Val	Arg
695	700	705
Val Gly Gly Phe Asp Val Ser Ile Gln	Gly Trp Gly Leu Glu	Asp
710	715	720
Val Asp Leu Phe Asn Lys Val Val Gln	Ala Gly Leu Lys Thr	Phe
725	730	735
Arg Ser Gln Glu Val Gly Val Val His	Val His His Pro Val	Phe
740	745	750
Cys Asp Pro Asn Leu Asp Pro Lys Gln	Tyr Lys Met Cys Leu	Gly
755	760	765
Ser Lys Ala Ser Thr Tyr Gly Ser Thr	Gln Gln Leu Ala Glu	Met
770	775	780
Trp Leu Glu Lys Asn Asp Pro Ser Tyr	Ser Lys Ser Ser Asn	Asn
785	790	795
Asn Gly Ser Val Arg Thr Ala		
800		

<210> 261
<211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 261
gtgccactac ggggtgtgga cgac 24

<210> 262
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 262
tcccatttct tccgtggtgc ccag 24

<210> 263
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 263
ccagaagaag tccttcatga tgctcaagta catgcacgac cactac 46

<210> 264
<211> 1419
<212> DNA
<213> Homo sapiens

<400> 264
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gttccggtcg catggcagag tgctacggac gacgcctatg aagcccttag 150
tccttctagt tgcgcttttg ctatggcctt cgtctgtgcc ggcttatccg 200
agcataactg tgacacctga tgaagagcaa aacttgaatc attatataca 250
agtttttagag aacctagtac gaagtgttcc ctctggggag ccaggtcgtg 300
agaaaaaatc taactctcca aaacatgttt attctatagc atcaaaggga 350
tcaaaattta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400

tgttttaacc aatcctatca gtgaagaaac tacaactttc cctacaggag 450
 gcttcacacc ggaaatagga aagaaaaaac acacggaaag taccctattc 500
 tggctgatca aaccaaacaa tgtttccatt gttttgcatg cagaggaacc 550
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 aaactgaggc accaagaatg ttgccagttg ttactgaatc atctacaagt 650
 ccatatgtta cctcatacaa gtcacctgtc accacttttag ataagagcac 700
 tggcattgag atctctacag aatcagaaga tgttcctcag ctctcaggtg 750
 aaactgcatg agaaaaaccc gaagagtttg gaaagcacc agagagttgg 800
 aataatgatg acattttgaa aaaaatttta gatattaatt cacaagtgca 850
 acaggcactt cttagtgaac ccagcaaccc agcatataga gaagatattg 900
 aagcctctaa agatcaccta aaacgaagcc ttgctctagc agcagcagca 950
 gaacataaat taaaaacaat gtataagtcc cagttattgc cagtaggacg 1000
 aacaagtaat aaaattgatg acatcgaaac tgttattaac atgctgtgta 1050
 attctagatc taaactctat gaatatttag atattaaatg tgttccacca 1100
 gagatgagag aaaaagctgc tacagtattc aatacattaa aaaatatgtg 1150
 tagatcaagg agagtcacag ccttattaaa agtttattaa acaataatat 1200
 aaaaatttta aacctacttg atattccata acaaagctga tttaagcaaa 1250
 ctgcattttt tcacaggaga aataatcata ttogtaattt caaaagttgt 1300
 ataaaaatat tttctattgt agttcaaagtg tgccaacatc tttatgtgtc 1350
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 attttggttc aggaaaaaa 1419

<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

Met	Lys	Pro	Leu	Val	Leu	Leu	Val	Ala	Leu	Leu	Leu	Trp	Pro	Ser
1				5					10					15

Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
				20					25					30

Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
				35					40					45

Ser	Val	Pro	Ser	Gly	Glu	Pro	Gly	Arg	Glu	Lys	Lys	Ser	Asn	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

				50					55					60
Pro	Lys	His	Val	Tyr	Ser	Ile	Ala	Ser	Lys	Gly	Ser	Lys	Phe	Lys
				65					70					75
Glu	Leu	Val	Thr	His	Gly	Asp	Ala	Ser	Thr	Glu	Asn	Asp	Val	Leu
				80					85					90
Thr	Asn	Pro	Ile	Ser	Glu	Glu	Thr	Thr	Thr	Phe	Pro	Thr	Gly	Gly
				95					100					105
Phe	Thr	Pro	Glu	Ile	Gly	Lys	Lys	Lys	His	Thr	Glu	Ser	Thr	Pro
				110					115					120
Phe	Trp	Ser	Ile	Lys	Pro	Asn	Asn	Val	Ser	Ile	Val	Leu	His	Ala
				125					130					135
Glu	Glu	Pro	Tyr	Ile	Glu	Asn	Glu	Glu	Pro	Glu	Pro	Glu	Pro	Glu
				140					145					150
Pro	Ala	Ala	Lys	Gln	Thr	Glu	Ala	Pro	Arg	Met	Leu	Pro	Val	Val
				155					160					165
Thr	Glu	Ser	Ser	Thr	Ser	Pro	Tyr	Val	Thr	Ser	Tyr	Lys	Ser	Pro
				170					175					180
Val	Thr	Thr	Leu	Asp	Lys	Ser	Thr	Gly	Ile	Glu	Ile	Ser	Thr	Glu
				185					190					195
Ser	Glu	Asp	Val	Pro	Gln	Leu	Ser	Gly	Glu	Thr	Ala	Ile	Glu	Lys
				200					205					210
Pro	Glu	Glu	Phe	Gly	Lys	His	Pro	Glu	Ser	Trp	Asn	Asn	Asp	Asp
				215					220					225
Ile	Leu	Lys	Lys	Ile	Leu	Asp	Ile	Asn	Ser	Gln	Val	Gln	Gln	Ala
				230					235					240
Leu	Leu	Ser	Asp	Thr	Ser	Asn	Pro	Ala	Tyr	Arg	Glu	Asp	Ile	Glu
				245					250					255
Ala	Ser	Lys	Asp	His	Leu	Lys	Arg	Ser	Leu	Ala	Leu	Ala	Ala	Ala
				260					265					270
Ala	Glu	His	Lys	Leu	Lys	Thr	Met	Tyr	Lys	Ser	Gln	Leu	Leu	Pro
				275					280					285
Val	Gly	Arg	Thr	Ser	Asn	Lys	Ile	Asp	Asp	Ile	Glu	Thr	Val	Ile
				290					295					300
Asn	Met	Leu	Cys	Asn	Ser	Arg	Ser	Lys	Leu	Tyr	Glu	Tyr	Leu	Asp
				305					310					315
Ile	Lys	Cys	Val	Pro	Pro	Glu	Met	Arg	Glu	Lys	Ala	Ala	Thr	Val
				320					325					330
Phe	Asn	Thr	Leu	Lys	Asn	Met	Cys	Arg	Ser	Arg	Arg	Val	Thr	Ala
				335					340					345

Leu Leu Lys Val Tyr
350

<210> 266

<211> 2403

<212> DNA

<213> Homo sapiens

<400> 266

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ttcatagtgt gagatcaacc cacaggaata tccatggctt ttgtgctcat 150
tttggttctc agtttctacg agctgggtgc aggacagtgg caagtcaactg 200
gaccgggcaa gtttgtccag gccttggtgg gggaggacgc cgtgttctcc 250
tgctccctct ttctgagac cagtgcagag gctatggaag tgcggttctt 300
caggaatcag ttccatgctg tggccacct ctacagagat ggggaagact 350
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ttccatccac cttgctgagc agagtcatga ggtggaatcc aaggatttga 800
taggagagac gtttttccag ccctcacctt ggcgcctggc ttctatttta 850
ctcgggttac tctgtgtgc cctgtgtggt gttgtcatgg ggatgataat 900
tgttttcttc aaatccaaag ggaaaatcca ggcggaactg gactggagaa 950
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tcacaggtga agattaaaga gacaacgaat gtgaatcatg cttgcagggt 1950
tgagggcaca gtgtttgcta atgatgtgtt tttatattat acattttccc 2000
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aatcaccca tggaatagtt attgaacacc tgctttgtga ggctcaaaga 2100
ataaagagga ggtaggattt ttcactgatt ctataagccc agcattacct 2150
gataccaaaa ccaggcaaag aaaacagaag aagaggaagg aaaactacag 2200
gtccatatcc ctcatataca cagacacaaa aattctaaat aaaattttta 2250
caaattaaac taaacaatat atttaaagat gatataatac tactcagtgt 2300
ggtttgtccc acaaatgcag agttggttta atatttaa atcaaccagt 2350
gtaattcagc acattaataa agtaaaaaag aaaaccataa aaaaaaaaaa 2400
aaa 2403

<210> 267
<211> 466
<212> PRT
<213> Homo sapiens

<400> 267
Met Ala Phe Val Leu Ile Leu Val Leu Ser Phe Tyr Glu Leu Val
1 5 10 15
Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala

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Leu Val Gly Glu Asp	Ala Val Phe Ser Cys	Ser Leu Phe Pro Glu			
	35		40		45
Thr Ser Ala Glu Ala	Met Glu Val Arg Phe	Phe Arg Asn Gln Phe			
	50		55		60
His Ala Val Val His	Leu Tyr Arg Asp Gly	Glu Asp Trp Glu Ser			
	65		70		75
Lys Gln Met Pro Gln	Tyr Arg Gly Arg Thr	Glu Phe Val Lys Asp			
	80		85		90
Ser Ile Ala Gly Gly	Arg Val Ser Leu Arg	Leu Lys Asn Ile Thr			
	95		100		105
Pro Ser Asp Ile Gly	Leu Tyr Gly Cys Trp	Phe Ser Ser Gln Ile			
	110		115		120
Tyr Asp Glu Glu Ala	Thr Trp Glu Leu Arg	Val Ala Ala Leu Gly			
	125		130		135
Ser Leu Pro Leu Ile	Ser Ile Val Gly Tyr	Val Asp Gly Gly Ile			
	140		145		150
Gln Leu Leu Cys Leu	Ser Ser Gly Trp Phe	Pro Gln Pro Thr Ala			
	155		160		165
Lys Trp Lys Gly Pro	Gln Gly Gln Asp Leu	Ser Ser Asp Ser Arg			
	170		175		180
Ala Asn Ala Asp Gly	Tyr Ser Leu Tyr Asp	Val Glu Ile Ser Ile			
	185		190		195
Ile Val Gln Glu Asn	Ala Gly Ser Ile Leu	Cys Ser Ile His Leu			
	200		205		210
Ala Glu Gln Ser His	Glu Val Glu Ser Lys	Val Leu Ile Gly Glu			
	215		220		225
Thr Phe Phe Gln Pro	Ser Pro Trp Arg Leu	Ala Ser Ile Leu Leu			
	230		235		240
Gly Leu Leu Cys Gly	Ala Leu Cys Gly Val	Val Met Gly Met Ile			
	245		250		255
Ile Val Phe Phe Lys	Ser Lys Gly Lys Ile	Gln Ala Glu Leu Asp			
	260		265		270
Trp Arg Arg Lys His	Gly Gln Ala Glu Leu	Arg Asp Ala Arg Lys			
	275		280		285
His Ala Val Glu Val	Thr Leu Asp Pro Glu	Thr Ala His Pro Lys			
	290		295		300
Leu Cys Val Ser Asp	Leu Lys Thr Val Thr	His Arg Lys Ala Pro			
	305		310		315

Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val	320	325	330
Val	Ala	Ser	Gln	Gly	Phe	Gln	Ala	Gly	Arg	His	Tyr	Trp	Glu	Val	335	340	345
Asp	Val	Gly	Gln	Asn	Val	Gly	Trp	Tyr	Val	Gly	Val	Cys	Arg	Asp	350	355	360
Asp	Val	Asp	Arg	Gly	Lys	Asn	Asn	Val	Thr	Leu	Ser	Pro	Asn	Asn	365	370	375
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Thr	Thr	Glu	His	Leu	Tyr	Phe	Thr	380	385	390
Phe	Asn	Pro	His	Phe	Ile	Ser	Leu	Pro	Pro	Ser	Thr	Pro	Pro	Thr	395	400	405
Arg	Val	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Gly	Gly	Thr	Ile	Ser	Phe	410	415	420
Phe	Asn	Thr	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Leu	Thr	Cys	425	430	435
Gln	Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Gln	His	Ala	Met	Tyr	440	445	450
Asp	Glu	Glu	Lys	Gly	Thr	Pro	Ile	Phe	Ile	Cys	Pro	Val	Ser	Trp	455	460	465

Gly

<210> 268
 <211> 2103
 <212> DNA
 <213> Homo sapiens

<400> 268
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 gtcattcttca tatccctgat tgtcctggca gtgtgcattg gactcactgt 150
 tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200
 tgtcattttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250
 aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300
 attttataaa tctccattaa gggaagaatt tgtcaagtct caggttatca 350
 agttcagtca acagaagcat ggagtgttgg ctcatatgct gttgatttgt 400
 agatttcact ctactgagga tcctgaaact gtagataaaa ttgttcaact 450
 tgttttacat gaaaagctgc aagatgctgt aggaccccct aaagtagatc 500

ctcactcagt taaaattaaa aaaatcaaca agacagaaac agacagctat 550
ctaaaccatt gctgcggaac acgaagaagt aaaactctag gtcagagtct 600
caggatcggt ggtgggacag aagtagaaga gggatgaatgg ccctggcagg 650
ctagcctgca gtgggatggg agtcatcgct gtggagcaac cttaattaat 700
gccacatggc ttgtgagtgc tgctcactgt tttacaacat ataagaaccc 750
tgccagatgg actgcttcct ttggagtaac aataaaacct tcgaaaatga 800
aacggggtct ccggagaata attgtccatg aaaaatacaa acacccatca 850
catgactatg atattttctt tgcagagctt tctagccctg ttccctacac 900
aatgcagta catagagttt gtctccctga tgcctcctat gagtttcaac 950
caggatgatg gatgtttgtg acaggatttg gagcactgaa aaatgatggg 1000
tacagtcaaa atcatcttcg acaagcacag gtgactctca tagacgctac 1050
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ggaggaccac tggtagttc agatgctaga gatattctgg accttgctgg 1200
aatagtgagc tggggagatg aatgtgcaa acccaacaag cctgggtgtt 1250
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cagaattttg acttggtgac ataaatttgt aatgcatata tacaatttga 1650
agcactcctt ttcttcagtt cctcagctcc tctcatttca gcaaatatcc 1700
attttcaagg tgcagaacaa ggagtgaag aaaatataag aagaaaaaaa 1750
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aatattagaa atgatcatat tcattatgaa aggtcaagca aagacagcag 1850
aataccaatc acttcatcat ttaggaagta tgggaactaa gttaaggaag 1900
tccagaaaga agccaagata tatccttatt ttcatttcca aacaactact 1950

atgataaatg tgaagaagat tctgtttttt tgtgacctat aataattata 2000
 caaacttcat gcaatgtact tgttctaagc aaattaaagc aaatatttat 2050
 ttaacattgt tactgaggat gtcaacatat aacaataaaa tataaatcac 2100
 cca 2103

<210> 269
 <211> 423
 <212> PRT
 <213> Homo sapiens

<400> 269
 Met Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys
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 Trp Glu Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile
 20 25 30
 Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr
 35 40 45
 Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr
 50 55 60
 Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn
 65 70 75
 Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala
 80 85 90
 Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val
 95 100 105
 Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu
 110 115 120
 Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp
 125 130 135
 Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val
 140 145 150
 Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile
 155 160 165
 Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr
 170 175 180
 Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly
 185 190 195
 Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln
 200 205 210
 Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr
 215 220 225

Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro
 230 235 240

Ala Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys
 245 250 255

Met Lys Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys
 260 265 270

His Pro Ser His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser
 275 280 285

Pro Val Pro Tyr Thr Asn Ala Val His Arg Val Cys Leu Pro Asp
 290 295 300

Ala Ser Tyr Glu Phe Gln Pro Gly Asp Val Met Phe Val Thr Gly
 305 310 315

Phe Gly Ala Leu Lys Asn Asp Gly Tyr Ser Gln Asn His Leu Arg
 320 325 330

Gln Ala Gln Val Thr Leu Ile Asp Ala Thr Thr Cys Asn Glu Pro
 335 340 345

Gln Ala Tyr Asn Asp Ala Ile Thr Pro Arg Met Leu Cys Ala Gly
 350 355 360

Ser Leu Glu Gly Lys Thr Asp Ala Cys Gln Gly Asp Ser Gly Gly
 365 370 375

Pro Leu Val Ser Ser Asp Ala Arg Asp Ile Trp Tyr Leu Ala Gly
 380 385 390

Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro Asn Lys Pro Gly
 395 400 405

Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile Thr Ser Lys
 410 415 420

Thr Gly Ile

<210> 270
 <211> 1170
 <212> DNA
 <213> Homo sapiens

<400> 270
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 cagacgtcag ctggtggatt cccgctgcat caaggcctac ccactgtctc 150
 catgctgggc tctccctgcc ttctgtggct cctggcogtg accttcttgg 200
 ttcccagagc tcagcccttg gccctcaag actttgaaga agaggaggca 250

Leu Ser Ser Pro Ala Gln Pro Pro Asp Pro Pro Arg Met Gly Glu
80 85 90

Val Arg Ile Ala Ala Glu Glu Gly Arg Ala Val Val His Trp Cys
95 100 105

Ala Pro Phe Ser Pro Val Leu His Tyr Trp Leu Leu Leu Trp Asp
110 115 120

Gly Ser Glu Ala Ala Gln Lys Gly Pro Pro Leu Asn Ala Thr Val
125 130 135

Arg Arg Ala Glu Leu Lys Gly Leu Lys Pro Gly Gly Ile Tyr Val
140 145 150

Val Cys Val Val Ala Ala Asn Glu Ala Gly Ala Ser Arg Val Pro
155 160 165

Gln Ala Gly Gly Glu Gly Leu Glu Gly Ala Asp Ile Pro Ala Phe
170 175 180

Gly Pro Cys Ser Arg Leu Ala Val Pro Pro Asn Pro Arg Thr Leu
185 190 195

Val His Ala Ala Val Gly Val Gly Thr Ala Leu Ala Leu Leu Ser
200 205 210

Cys Ala Ala Leu Val Trp His Phe Cys Leu Arg Asp Arg Trp Gly
215 220 225

Cys Pro Arg Arg Ala Ala Ala Arg Ala Ala Gly Ala Leu
230 235

<210> 272
<211> 2397
<212> DNA
<213> Homo sapiens

<400> 272
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cccaggcggg cgtggggcac cgggccacgc gccgacgac gctgccgttt 150
tgcccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg 200
gctcacaatg gccagagaag attccgtgaa gtgtctgcgc tgctgtctct 250
acgccctcaa tctgctcttt tggttaaatgt ccatcagtgt gttggcagtt 300
tctgcttggg tgagggaacta cctaaataat gttctcactt taactgcaga 350
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cggatcatgat tgctgtttgc tgtttcctta tcattgtggg gatgttagga 450
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aagtttgctt gtcattttct gtgtagaact ggcttgtggc gtttggacat 550
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aaagccagga tgacaaatta tggattacct agatatcggt ggcttactca 650
tgcttggaaat ttttttcaga gagagttaa gtgctgtgga gtagtatatt 700
tactgactg gttggaaatg acagagatgg actggccccc agattcctgc 750
tgtgttagag aattcccagg atgttccaaa caggcccacc aggaagatct 800
cagtgcctt tatcaagagg gttgtgggaa gaaaatgtat tcctttttga 850
gaggaaccaa acaactgcag gtgctgaggt ttctgggaat ctccattggg 900
gtgacacaaa tcctggccat gattctcacc attactctgc tctgggctct 950
gtattatgat agaaggagc ctgggacaga ccaaatgatg tccttgaaga 1000
atgacaactc tcagcacctg tcatgtccct cagtagaact gttgaaacca 1050
agcctgtcaa gaatctttga acacacatcc atggcaaaca gctttaatac 1100
acactttgag atggaggagt tataaaaaga aatgtcacag aagaaaacca 1150
caaacttggt ttattggact tgtgaatttt tgagtacata ctatgtgttt 1200
cagaaatatg tagaaataaa aatgttgcca taaaataaca cctaagcata 1250
tactattcta tgctttaaaa tgaggatgga aaagtttcat gtcataagtc 1300
accacctgga caataattga tgcccttaaa atgctgaaga cagatgtcat 1350
accactgtg tagcctgtgt atgactttta ctgaacacag ttatgttttg 1400
aggcagcatg gtttgattag catttccgca tccatgcaaa cgagtcacat 1450
atggtgggac tggagccata gtaaaggttg atttacttct accaactagt 1500
atataaagta ctaattaaat gctaacatag gaagttagaa aatactaata 1550
acttttatta ctacgcgac tattcttctg atgctaaata aattatatat 1600
cagaaaactt tcaatattgg tgactaccta aatgtgattt ttgctgggta 1650
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actattctgt cctgggctta tattacacat ataactgtta tttaaatact 1900
taaccactaa ttttgaaaat taccagtgtg atacatagga atcattattc 1950

agaatgtagt ctggtcttta ggaagtatta ataagaaaat ttgcacataa 2000
 cttagttgat tcagaaagga cttgtatgct gtttttctcc caaatgaaga 2050
 ctctttttga cactaaacac tttttaaaaa gcttatcttt gccttctcca 2100
 aacaagaagc aatagtctcc aagtcaatat aaattctaca gaaaatagtg 2150
 ttctttttct ccagaaaaat gcttgtgaga atcattaaaa catgtgacaa 2200
 tttagagatt ctttgtttta tttcactgat taatatactg tggcaaatta 2250
 cacagattat taaatttttt tacaagagta tagtatattt atttgaaatg 2300
 ggaaaagtgc attttactgt attttgtgta ttttgtttat ttctcagaat 2350
 atggaaagaa aattaataatg tgtcaataaa tattttctag agagtaa 2397

<210> 273
 <211> 305
 <212> PRT
 <213> Homo sapiens

<400> 273
 Met Ala Arg Glu Asp Ser Val Lys Cys Leu Arg Cys Leu Leu Tyr
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 Ala Leu Asn Leu Leu Phe Trp Leu Met Ser Ile Ser Val Leu Ala
 20 25 30
 Val Ser Ala Trp Met Arg Asp Tyr Leu Asn Asn Val Leu Thr Leu
 35 40 45
 Thr Ala Glu Thr Arg Val Glu Glu Ala Val Ile Leu Thr Tyr Phe
 50 55 60
 Pro Val Val His Pro Val Met Ile Ala Val Cys Cys Phe Leu Ile
 65 70 75
 Ile Val Gly Met Leu Gly Tyr Cys Gly Thr Val Lys Arg Asn Leu
 80 85 90
 Leu Leu Leu Ala Trp Tyr Phe Gly Ser Leu Leu Val Ile Phe Cys
 95 100 105
 Val Glu Leu Ala Cys Gly Val Trp Thr Tyr Glu Gln Glu Leu Met
 110 115 120
 Val Pro Val Gln Trp Ser Asp Met Val Thr Leu Lys Ala Arg Met
 125 130 135
 Thr Asn Tyr Gly Leu Pro Arg Tyr Arg Trp Leu Thr His Ala Trp
 140 145 150
 Asn Phe Phe Gln Arg Glu Phe Lys Cys Cys Gly Val Val Tyr Phe
 155 160 165
 Thr Asp Trp Leu Glu Met Thr Glu Met Asp Trp Pro Pro Asp Ser

	170		175		180
Cys Cys Val Arg	Glu Phe Pro Gly Cys	Ser Lys Gln Ala His Gln			
	185	190			195
Glu Asp Leu Ser	Asp Leu Tyr Gln Glu	Gly Cys Gly Lys Lys Met			
	200	205			210
Tyr Ser Phe Leu	Arg Gly Thr Lys Gln	Leu Gln Val Leu Arg Phe			
	215	220			225
Leu Gly Ile Ser	Ile Gly Val Thr Gln	Ile Leu Ala Met Ile Leu			
	230	235			240
Thr Ile Thr Leu	Leu Trp Ala Leu Tyr	Tyr Asp Arg Arg Glu Pro			
	245	250			255
Gly Thr Asp Gln	Met Met Ser Leu Lys	Asn Asp Asn Ser Gln His			
	260	265			270
Leu Ser Cys Pro	Ser Val Glu Leu Leu	Lys Pro Ser Leu Ser Arg			
	275	280			285
Ile Phe Glu His	Thr Ser Met Ala Asn	Ser Phe Asn Thr His Phe			
	290	295			300
Glu Met Glu Glu	Leu				
	305				

<210> 274
 <211> 2063
 <212> DNA
 <213> Homo sapiens

<400> 274
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 cttgggggtga caatctcagc tccaggctac agggagaccg ggaggatcac 200
 agagccagca tgttacagga tcctgacagt gatcaacctc tgaacagcct 250
 cgatgtcaaa ccctgcgcga aaccccgat ccccatggag accttcagaa 300
 aggtggggat ccccatcatc atagcactac tgagcctggc gagtatcatc 350
 attgtggttg tcctcatcaa ggtgattctg gataaatact acttcctctg 400
 cgggcagcct ctccacttca tcccaggaa gcagctgtgt gacggagagc 450
 tggactgtcc cttgggggag gacgaggagc actgtgtcaa gagcttcccc 500
 gaagggcctg cagtggcagt ccgcctctcc aaggaccgat ccacactgca 550
 ggtgctggac tcggccacag ggaactgggt ctctgcctgt ttcgacaact 600

tcacagaagc tctcgtgag acagcctgta ggcagatggg ctacagcaga 650
 gctgtggaga ttggcccaga ccaggatctg gatgttggtg aaatcacaga 700
 aaacagccag gagcttcgca tgcggaactc aagtggggcc tgtctctcag 750
 gctccctggg ctccctgcac tgtcttgccg gtgggaagag cctgaagacc 800
 ccccggtgtg tgggtgggga ggaggcctct gtggattctt ggccttggca 850
 ggtcagcatc cagtacgaca aacagcacgt ctgtggaggg agcatcctgg 900
 acccccactg ggtcctcacg gcagcccact gcttcaggaa acataccgat 950
 gtgttcaact ggaaggtgcg ggcaggctca gacaaactgg gcagcttccc 1000
 atccctgggt gtggccaaga tcatcatcat tgaattcaac cccatgtacc 1050
 ccaaagacaa tgacatcgcc ctcatgaagc tgcagttccc actcactttc 1100
 tcaggcacag tcaggcccat ctgtctgccc ttctttgatg aggagctcac 1150
 tccagccacc cactctgga tcattggatg gggctttacg aagcagaatg 1200
 gaggggaagat gtctgacata ctgctgcagg cgtcagtcca ggtcattgac 1250
 agcacacggt gcaatgcaga cgatgcgtac cagggggaag tcaccgagaa 1300
 gatgatgtgt gcaggcatcc cggaaggggg tgtggacacc tgccaggggtg 1350
 acagtgggtg gccctgatg taccaatctg accagtggca tgtggtgggc 1400
 atcgttagct ggggctatgg ctgcgggggc ccgagcacco caggagtata 1450
 caccaaggtc tcagcctatc tcaactggat ctacaatgtc tggaaggctg 1500
 agctgtaatg ctgctgcccc ttgacagtgc tgggagccgc ttccttcctg 1550
 ccctgcccac ctggggatcc ccaaagtca gacacagagc aagagtcccc 1600
 ttgggtacac ccctctgccc acagcctcag cattttcttg agcagcaaag 1650
 ggcctcaatt cctgtaagag accctcgag cccagaggcg cccagaggaa 1700
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 aactttccca cactactgaa tggaagcagg ctgtcttgta aaagcccaga 1850
 tcaactgtgg ctggagagga gaaggaaagg gtctgcgcca gccctgtccg 1900
 tcttcaccca tcccgaagcc tactagagca agaaaccagt tgtaataata 1950
 aatgcactgc cctactgttg gtatgactac cgttacctac tgttgtcatt 2000
 gttattacag ctatggccac tattattaaa gagctgtgta acatctctgg 2050

caaaaaaaaaaaa aaa 2063

<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

Met	Leu	Gln	Asp	Pro	Asp	Ser	Asp	Gln	Pro	Leu	Asn	Ser	Leu	Asp
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Val	Lys	Pro	Leu	Arg	Lys	Pro	Arg	Ile	Pro	Met	Glu	Thr	Phe	Arg
				20					25					30
Lys	Val	Gly	Ile	Pro	Ile	Ile	Ile	Ala	Leu	Leu	Ser	Leu	Ala	Ser
				35					40					45
Ile	Ile	Ile	Val	Val	Val	Leu	Ile	Lys	Val	Ile	Leu	Asp	Lys	Tyr
				50					55					60
Tyr	Phe	Leu	Cys	Gly	Gln	Pro	Leu	His	Phe	Ile	Pro	Arg	Lys	Gln
				65					70					75
Leu	Cys	Asp	Gly	Glu	Leu	Asp	Cys	Pro	Leu	Gly	Glu	Asp	Glu	Glu
				80					85					90
His	Cys	Val	Lys	Ser	Phe	Pro	Glu	Gly	Pro	Ala	Val	Ala	Val	Arg
				95					100					105
Leu	Ser	Lys	Asp	Arg	Ser	Thr	Leu	Gln	Val	Leu	Asp	Ser	Ala	Thr
				110					115					120
Gly	Asn	Trp	Phe	Ser	Ala	Cys	Phe	Asp	Asn	Phe	Thr	Glu	Ala	Leu
				125					130					135
Ala	Glu	Thr	Ala	Cys	Arg	Gln	Met	Gly	Tyr	Ser	Arg	Ala	Val	Glu
				140					145					150
Ile	Gly	Pro	Asp	Gln	Asp	Leu	Asp	Val	Val	Glu	Ile	Thr	Glu	Asn
				155					160					165
Ser	Gln	Glu	Leu	Arg	Met	Arg	Asn	Ser	Ser	Gly	Pro	Cys	Leu	Ser
				170					175					180
Gly	Ser	Leu	Val	Ser	Leu	His	Cys	Leu	Ala	Cys	Gly	Lys	Ser	Leu
				185					190					195
Lys	Thr	Pro	Arg	Val	Val	Gly	Gly	Glu	Glu	Ala	Ser	Val	Asp	Ser
				200					205					210
Trp	Pro	Trp	Gln	Val	Ser	Ile	Gln	Tyr	Asp	Lys	Gln	His	Val	Cys
				215					220					225
Gly	Gly	Ser	Ile	Leu	Asp	Pro	His	Trp	Val	Leu	Thr	Ala	Ala	His
				230					235					240
Cys	Phe	Arg	Lys	His	Thr	Asp	Val	Phe	Asn	Trp	Lys	Val	Arg	Ala
				245					250					255

Gly Ser Asp Lys	Leu Gly Ser Phe Pro Ser Leu Ala Val Ala Lys	260	265	270
Ile Ile Ile Ile	Glu Phe Asn Pro Met Tyr Pro Lys Asp Asn Asp	275	280	285
Ile Ala Leu Met	Lys Leu Gln Phe Pro Leu Thr Phe Ser Gly Thr	290	295	300
Val Arg Pro Ile	Cys Leu Pro Phe Phe Asp Glu Glu Leu Thr Pro	305	310	315
Ala Thr Pro Leu	Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln Asn	320	325	330
Gly Gly Lys Met	Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val	335	340	345
Ile Asp Ser Thr	Arg Cys Asn Ala Asp Asp Ala Tyr Gln Gly Glu	350	355	360
Val Thr Glu Lys	Met Met Cys Ala Gly Ile Pro Glu Gly Gly Val	365	370	375
Asp Thr Cys Gln	Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser	380	385	390
Asp Gln Trp His	Val Val Gly Ile Val Ser Trp Gly Tyr Gly Cys	395	400	405
Gly Gly Pro Ser	Thr Pro Gly Val Tyr Thr Lys Val Ser Ala Tyr	410	415	420
Leu Asn Trp Ile	Tyr Asn Val Trp Lys Ala Glu Leu	425	430	

<210> 276
 <211> 3143
 <212> DNA
 <213> Homo sapiens

<400> 276
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 gagcatggcc ctcccagccc tgggcctgga cccctggagc ctctggggcc 150
 ttttctctt ccaactgctt cagctgctgc tgccgacgac gaccgcgggg 200
 ggaggcgggc agggggccat gccagggtc agatactatg caggggatga 250
 acgtagggca cttagcttct tccaccagaa gggcctccag gattttgaca 300
 ctctgctcct gagtggatg gaaatactc tctacgtggg ggctcgagaa 350
 gccattctgg ccttgatata ccaggatcca ggggtcccca ggctaaagaa 400

[illegible]

ctgtcagcct tggcctctta ttattggagt catggcccag cagcagtccc 1900
agaagcctct tccactgtct acaatggctc cctcttgctg atagtgcagg 1950
atggagttgg gggctcttac cagtgcctgg caactgagaa tggcttttca 2000
taccctgtga tctctactg ggtggacagc caggaccaga ccctggccct 2050
ggatcctgaa ctggcaggca tccccggga gcatgtgaag gtcccgttga 2100
ccagggtcag tgggtggggcc gccctggctg cccagcagtc ctactggccc 2150
cactttgtca ctgtcactgt cctctttgcc ttagtgcttt caggagccct 2200
catcatcctc gtggcctccc cattgagagc actccgggct cggggcaagg 2250
ttcagggtg tgagaccctg cgcctgggg agaaggcccc gttaagcaga 2300
gagcaacacc tccagtctcc caaggaatgc aggacctctg ccagtgatgt 2350
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caggccgggg ctgcggtgca ggcacctggc catgctggct gggcggccca 2450
agcacagccc tgactaggat gacagcagca caaaagacca cctttctccc 2500
ctgagaggag cttctgctac tctgcatcac tgatgacact cagcagggtg 2550
atgcacagca gtctgcctcc cctatgggac tccctttctac caagcacatg 2600
agctctctaa cagggtgggg gctaccccca gacctgctcc tacactgata 2650
ttgaagaacc tggagaggat ccttcagttc tggccattcc agggaccctc 2700
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cctatggtaa tgaacaccaa acatctaaac aatcatatgc taacatgcc 2800
ctcctggaaa ctccactctg aagctgccgc tttggacacc aacactccct 2850
tctcccagg tcatgcagg atctgctccc tctgcttcc cttaccagtc 2900
gtgcaccgct gactcccagg aagtctttcc tgaagtctga ccacctttct 2950
tcttgcttca gttggggcag actctgatcc cttctgccct ggcagaatgg 3000
caggggtaat ctgagccttc ttcactcctt taccctagct gacccttca 3050
cctctcccc tcccttttcc tttgttttg gattcagaaa actgcttgtc 3100
agagactgtt tattttttat taaaaatata aggttaaaaa aaa 3143

<210> 277
<211> 761
<212> PRT
<213> Homo sapiens
<400> 277

Met	Ala	Leu	Pro	Ala	Leu	Gly	Leu	Asp	Pro	Trp	Ser	Leu	Leu	Gly	1	5	10	15
Leu	Phe	Leu	Phe	Gln	Leu	Leu	Gln	Leu	Leu	Leu	Pro	Thr	Thr	Thr	20	25	30	
Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr	35	40	45	
Ala	Gly	Asp	Glu	Arg	Arg	Ala	Leu	Ser	Phe	Phe	His	Gln	Lys	Gly	50	55	60	
Leu	Gln	Asp	Phe	Asp	Thr	Leu	Leu	Leu	Ser	Gly	Asp	Gly	Asn	Thr	65	70	75	
Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Ile	Leu	Ala	Leu	Asp	Ile	Gln	80	85	90	
Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala	95	100	105	
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn	110	115	120	
Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn	125	130	135	
Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala	140	145	150	
Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser	155	160	165	
Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro	170	175	180	
Ala	His	Lys	His	Thr	Ala	Val	Leu	Val	Asp	Gly	Met	Leu	Tyr	Ser	185	190	195	
Gly	Thr	Met	Asn	Asn	Phe	Leu	Gly	Ser	Glu	Pro	Ile	Leu	Met	Arg	200	205	210	
Thr	Leu	Gly	Ser	Gln	Pro	Val	Leu	Lys	Thr	Asp	Asn	Phe	Leu	Arg	215	220	225	
Trp	Leu	His	His	Asp	Ala	Ser	Phe	Val	Ala	Ala	Ile	Pro	Ser	Thr	230	235	240	
Gln	Val	Val	Tyr	Phe	Phe	Phe	Glu	Glu	Thr	Ala	Ser	Glu	Phe	Asp	245	250	255	
Phe	Phe	Glu	Arg	Leu	His	Thr	Ser	Arg	Val	Ala	Arg	Val	Cys	Lys	260	265	270	
Asn	Asp	Val	Gly	Gly	Glu	Lys	Leu	Leu	Gln	Lys	Lys	Trp	Thr	Thr	275	280	285	
Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Thr	Gln	Pro	Gly	Gln	Leu	Pro				

290	295	300
Phe Asn Val Ile Arg His Ala Val Leu	Leu Pro Ala Asp Ser Pro	
305	310	315
Thr Ala Pro His Ile Tyr Ala Val Phe	Thr Ser Gln Trp Gln Val	
320	325	330
Gly Gly Thr Arg Ser Ser Ala Val Cys	Ala Phe Ser Leu Leu Asp	
335	340	345
Ile Glu Arg Val Phe Lys Gly Lys Tyr	Lys Glu Leu Asn Lys Glu	
350	355	360
Thr Ser Arg Trp Thr Thr Tyr Arg Gly	Pro Glu Thr Asn Pro Arg	
365	370	375
Pro Gly Ser Cys Ser Val Gly Pro Ser	Ser Asp Lys Ala Leu Thr	
380	385	390
Phe Met Lys Asp His Phe Leu Met Asp	Glu Gln Val Val Gly Thr	
395	400	405
Pro Leu Leu Val Lys Ser Gly Val Glu	Tyr Thr Arg Leu Ala Val	
410	415	420
Glu Thr Ala Gln Gly Leu Asp Gly His	Ser His Leu Val Met Tyr	
425	430	435
Leu Gly Thr Thr Thr Gly Ser Leu His	Lys Ala Val Val Ser Gly	
440	445	450
Asp Ser Ser Ala His Leu Val Glu Glu	Ile Gln Leu Phe Pro Asp	
455	460	465
Pro Glu Pro Val Arg Asn Leu Gln Leu	Ala Pro Thr Gln Gly Ala	
470	475	480
Val Phe Val Gly Phe Ser Gly Gly Val	Trp Arg Val Pro Arg Ala	
485	490	495
Asn Cys Ser Val Tyr Glu Ser Cys Val	Asp Cys Val Leu Ala Arg	
500	505	510
Asp Pro His Cys Ala Trp Asp Pro Glu	Ser Arg Thr Cys Cys Leu	
515	520	525
Leu Ser Ala Pro Asn Leu Asn Ser Trp	Lys Gln Asp Met Glu Arg	
530	535	540
Gly Asn Pro Glu Trp Ala Cys Ala Ser	Gly Pro Met Ser Arg Ser	
545	550	555
Leu Arg Pro Gln Ser Arg Pro Gln Ile	Ile Lys Glu Val Leu Ala	
560	565	570
Val Pro Asn Ser Ile Leu Glu Leu Pro	Cys Pro His Leu Ser Ala	
575	580	585

Leu Ala Ser Tyr Tyr Trp Ser His Gly Pro Ala Ala Val Pro Glu
590 595 600

Ala Ser Ser Thr Val Tyr Asn Gly Ser Leu Leu Leu Ile Val Gln
605 610 615

Asp Gly Val Gly Gly Leu Tyr Gln Cys Trp Ala Thr Glu Asn Gly
620 625 630

Phe Ser Tyr Pro Val Ile Ser Tyr Trp Val Asp Ser Gln Asp Gln
635 640 645

Thr Leu Ala Leu Asp Pro Glu Leu Ala Gly Ile Pro Arg Glu His
650 655 660

Val Lys Val Pro Leu Thr Arg Val Ser Gly Gly Ala Ala Leu Ala
665 670 675

Ala Gln Gln Ser Tyr Trp Pro His Phe Val Thr Val Thr Val Leu
680 685 690

Phe Ala Leu Val Leu Ser Gly Ala Leu Ile Ile Leu Val Ala Ser
695 700 705

Pro Leu Arg Ala Leu Arg Ala Arg Gly Lys Val Gln Gly Cys Glu
710 715 720

Thr Leu Arg Pro Gly Glu Lys Ala Pro Leu Ser Arg Glu Gln His
725 730 735

Leu Gln Ser Pro Lys Glu Cys Arg Thr Ser Ala Ser Asp Val Asp
740 745 750

Ala Asp Asn Asn Cys Leu Gly Thr Glu Val Ala
755 760

<210> 278
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 278
ctgctggtga aatctggcgt ggag 24

<210> 279
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 279
gtctggtcct ggctgtccac ccag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 280
catcttgtca tgtacctggg aaccaccaca gggtcgctcc acaag 45

<210> 281
<211> 2320
<212> DNA
<213> Homo sapiens

<400> 281
aggggtccctt agccgggagc agggcgcgca gccagggctg agatccgagg 50
cttccgtaga agtgagcatg gctgggcagc gagtgcttct tctagtgggc 100
ttccttctcc ctggggctct gctctcagag gctgccaaaa tcttgacaat 150
atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200
ttcttcaaga tcacgggcat aatgtcacca tgcttaacca caaaagaggt 250
ccttttatgc cagattttta aaaggaagaa aaatcatatc aagttatcag 300
ttggcttgca cctgaagatc atcaaagaga atttaaaaag agttttgatt 350
tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400
aatgttctag aatacttggc gttgcagtgc agtcattttt taaatagaaa 450
ggatatcatg gattccttaa agaagagaaa cttagacatg gtgatagttg 500
aaacttttga ctactgtcct ttcttgattg ctgagaagct tgggaagcca 550
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aatccccttg tcttatgttc cagtattcog ttcttgctg actgatcaca 650
tggacttctg gggccgagtg aagaattttc tgatgttctt tagtttctgc 700
aggaggcaac agcacatgca gtctacattt gacaacacca tcaaggaaca 750
tttcacagaa ggctctaggc cagttttgtc tcatcttcta ctgaaagcag 800
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cttccaaca ctgtttatgt tggaggcttg atggaaaaac ctattaaacc 900

<210> 282
 <211> 523
 <212> PRT
 <213> Homo sapiens

<400> 282

Met	Ala	Gly	Gln	Arg	Val	Leu	Leu	Leu	Val	Gly	Phe	Leu	Leu	Pro
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Gly	Val	Leu	Leu	Ser	Glu	Ala	Ala	Lys	Ile	Leu	Thr	Ile	Ser	Thr
				20					25					30
Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ser	Gln	Ile
				35					40					45
Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	His	Lys	Arg
				50					55					60
Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Ser	Tyr	Gln
				65					70					75
Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Glu	Phe	Lys
				80					85					90
Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly	Arg	Gly
				95					100					105
Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Ala	Leu	Gln
				110					115					120
Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Ser	Leu	Lys
				125					130					135
Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Asp	Tyr	Cys
				140					145					150
Pro	Phe	Leu	Ile	Ala	Glu	Lys	Leu	Gly	Lys	Pro	Phe	Val	Ala	Ile
				155					160					165
Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro	Ile	Pro
				170					175					180
Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Asp	His	Met
				185					190					195
Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	Ser	Phe
				200					205					210
Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr	Ile
				215					220					225
Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His	Leu
				230					235					240
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe	Ala	Phe
				245					250					255
Asp	Phe	Ala	Arg	Pro	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Val	Gly	Gly

260	265	270
Leu Met Glu Lys Pro Ile Lys Pro Val	Pro Gln Asp Leu Glu Asn	
275	280	285
Phe Ile Ala Lys Phe Gly Asp Ser Gly	Phe Val Leu Val Thr Leu	
290	295	300
Gly Ser Met Val Asn Thr Cys Gln Asn	Pro Glu Ile Phe Lys Glu	
305	310	315
Met Asn Asn Ala Phe Ala His Leu Pro	Gln Gly Val Ile Trp Lys	
320	325	330
Cys Gln Cys Ser His Trp Pro Lys Asp	Val His Leu Ala Ala Asn	
335	340	345
Val Lys Ile Val Asp Trp Leu Pro Gln	Ser Asp Leu Leu Ala His	
350	355	360
Pro Ser Ile Arg Leu Phe Val Thr His	Gly Gly Gln Asn Ser Ile	
365	370	375
Met Glu Ala Ile Gln His Gly Val Pro	Met Val Gly Ile Pro Leu	
380	385	390
Phe Gly Asp Gln Pro Glu Asn Met Val	Arg Val Glu Ala Lys Lys	
395	400	405
Phe Gly Val Ser Ile Gln Leu Lys Lys	Leu Lys Ala Glu Thr Leu	
410	415	420
Ala Leu Lys Met Lys Gln Ile Met Glu	Asp Lys Arg Tyr Lys Ser	
425	430	435
Ala Ala Val Ala Ala Ser Val Ile Leu	Arg Ser His Pro Leu Ser	
440	445	450
Pro Thr Gln Arg Leu Val Gly Trp Ile	Asp His Val Leu Gln Thr	
455	460	465
Gly Gly Ala Thr His Leu Lys Pro Tyr	Val Phe Gln Gln Pro Trp	
470	475	480
His Glu Gln Tyr Leu Phe Asp Val Phe	Val Phe Leu Leu Gly Leu	
485	490	495
Thr Leu Gly Thr Leu Trp Leu Cys Gly	Lys Leu Leu Gly Met Ala	
500	505	510
Val Trp Trp Leu Arg Gly Ala Arg Lys	Val Lys Glu Thr	
515	520	

<210> 283
 <211> 24
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 283
tgcctttgct cacctacccc aagg 24

<210> 284
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 284
tcaggctggt ctccaaagag aggg 24

<210> 285
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 285
cccaaagatg tccacctggc tgcaaattgtg aaaattgtgg actgg 45

<210> 286
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 286
gggctgttga tttgtggggg attttgaaga gaggaggaat aggaggaagg 50
ggttgagggg ctgcctctgg catatgcaca cactcacaca ttctgtcaca 100
cccgtcacac acacatacca tgttctccat cccccaggt ccagccctca 150
gtgctgtccc atccagcagg gctaccctga agctctggct gcagccctcc 200
cgtccagtgg gcaggcggct tcatccctcc tttctctccc aaagcccaac 250
tgctgtcact gcatgctctg ccaaggagga gggaactgca gtgacagcag 300
gagtaagagt gggaggcagg acagagctgg gacacaggta tggagagggg 350
gttcagcgag cctagagagg gcagactatc aggggtgccg cggtgagaat 400
ccagggagag gagcggaaac agaagagggg cagaagaccg gggcacttgt 450

ggggtgcaga gccctcagc catgttggga gccaaagccac actggctacc 500
 aggtccccta cacagtcccg ggctgccctt ggttctggtg cttctggccc 550
 tgggggcccgg gtggggccag gaggggtcag agcccgtoct gctggagggg 600
 gagtgcctgg tggctctgtg gccctggccga gctgctgcag gggggcccgg 650
 gggagcagcc ctgggagagg caccctctgg gcgagtggca tttgctgcgg 700
 tccgaagcca ccaccatgag ccagcagggg aaaccggcaa tggcaccagt 750
 ggggccatct acttcgacca ggtcctggtg aacgagggcg gtggctttga 800
 ccgggcctct ggctccttcg tagccctgt cgggggtgtc tacagcttcc 850
 ggttccatgt ggtgaagggt tacaaccgcc aaactgtcca ggtgagcctg 900
 atgctgaaca cgtggcctgt catctcagcc tttgccaatg atcctgacgt 950
 gaccgggag gcagccacca gctctgtgct actgcccttg gaccctgggg 1000
 accgagtgtc tctgcgcctg cgtcggggga atctactggg tggttggaaa 1050
 tactcaagtt tctctggctt cctcatcttc cctctctgag gacccaagtc 1100
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 cccagaaac agcagaggca ggagagagac tccctctggc tcctatccca 1200
 cctctttgca tgggaccctg tgccaaacac ccaagtttaa gagaagagta 1250
 gagctgtggc atctccagac caggcctttc caccaccca ccccagtta 1300
 ccctcccagc cacctgctgc atctgttctt gcctgcagcc ctaggatcag 1350
 ggcaaggttt ggcaagaagg aagatctgca ctactttgag gcctctgctc 1400
 ctccggttcc cccaccccag ctctctgctc aatgctgac agggacaggt 1450
 ggcgcagggtg agcctgacag gccccacag gagcccagat ggacaagcct 1500
 cagcgtaccc tgcaggcttc ttctgtgag gaaagccagc atcacggatc 1550
 tcagccagca ccgtcagaag ctgagccagc accgtatggg ctaggggtggg 1600
 aggctcagcc acaggcagaa gggtggggaag ggcttgaggt ctgtggctgg 1650
 tgaggaagga aggaggggtg attgtctaga ctgaacatgg tacacattct 1700
 gcatgtatag cagagcagcc agcaggtagc aatcctggct gtccttctat 1750
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 tgagtgtgtt tgctctggct gagagcagag ctgagagcag gtatacagag 1850
 ctggaagtgg accatggaaa acatcgataa ccatgcatcc tcttgcttgg 1900

ccacctcctg aaactgctcc acctttgaag tttgaacttt agtccctcca 1950
 cactctgact gctgcctcct tcctcccagc tctctcactg agttatcttc 2000
 actgtacctg ttccagcata tccccactat ctctctttct cctgatctgt 2050
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 cattccttca gaccctctcc tgccagtatg ctaaaccctc cctctctctt 2150
 tcttatcccg ctgtcccatt ggcccagcct ggatgaatct atcaataaaa 2200
 caactagaga atgggtgtca gtgagacact atagaattac taaggagaag 2250
 atgcctctgg agtttggatc ggggtgtaca ggtacaagta ggtatgttgc 2300
 agaggaaaat aaatatcaaa ctgtatacta aaattaaaaa 2340

<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

Met	Leu	Gly	Ala	Lys	Pro	His	Trp	Leu	Pro	Gly	Pro	Leu	His	Ser
1				5					10					15
Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly
				20					25					30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
				35					40					45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
				50					55					60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
				65					70					75
Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn
				80					85					90
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu
				95					100					105
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val
				110					115					120
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn
				125					130					135
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val
				140					145					150
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala
				155					160					165
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser

ttcccgcggg gccgtgactg ggcggggcttc agccatgaag accctcatag 200
 ccgcctactc cgggggtcctg cgcgggcgagc gtcaggccga ggctgaccgg 250
 agccagcgct ctcacggagg acctgogctg tcgcgcgagg ggtctgggag 300
 atgggggcaact ggatccagca tcctctcogc cctccaggac ctcttctctg 350
 tcacctgggt caataggtcc aaggtggaaa agcagctaca ggtcatctca 400
 gtgctccagt ggggtcctgtc cttccttgta ctgggagtgg cctgcagtgc 450
 catcctcatg tacatattct gcaactgattg ctggctcatc gctgtgctct 500
 acttcacttg gctgggtgttt gactggaaca cacccaagaa aggtggcagg 550
 aggtcacagt ggggtccgaaa ctgggctgtg tggcgctact ttcgagacta 600
 ctttcccatc cagctgggtga agacacacaa cctgctgacc accaggaact 650
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 agtacctgat gtctggaggt atctgccctg tcagccggga caccatagac 850
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 ctggttccca tctactcctt tggagagaat gaagtgtaca agcaggtgat 1050
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 aaaaaaaaaa aaaaaaaaaa 1570

<210> 292
 <211> 388
 <212> PRT
 <213> Homo sapiens

<400> 292

Met	Lys	Thr	Leu	Ile	Ala	Ala	Tyr	Ser	Gly	Val	Leu	Arg	Gly	Glu	1	5	10	15
Arg	Gln	Ala	Glu	Ala	Asp	Arg	Ser	Gln	Arg	Ser	His	Gly	Gly	Pro	20	25	30	
Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser	35	40	45	
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn	50	55	60	
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln	65	70	75	
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile	80	85	90	
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu	95	100	105	
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly	110	115	120	
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr	125	130	135	
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu	140	145	150	
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile	155	160	165	
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu	170	175	180	
Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu	Ala	Thr	Leu	185	190	195	
Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu	Met	Ser	200	205	210	
Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu	215	220	225	
Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly	230	235	240	
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr	245	250	255	
Leu	Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly				

260	265	270
Ala Asp Leu Val Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr		
275	280	285
Lys Gln Val Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln		
290	295	300
Lys Lys Phe Gln Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His		
305	310	315
Gly Arg Gly Leu Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr		
320	325	330
Ser Lys Pro Ile Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro		
335	340	345
Lys Leu Glu His Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr		
350	355	360
Met Tyr Met Glu Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr		
365	370	375
Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu Val Asn		
380	385	

<210> 293
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 293
 gctgacctgg ttcccatcta ctcc 24

<210> 294
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 294
 cccacagaca cccatgacac ttcc 24

<210> 295
 <211> 50
 <212> DNA
 <213> Artificial

<220>

<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 295
aagaatgaat tgtacaaagc aggtgatcctt cgaggagggc tcctggggcc 50

<210> 296
<211> 3060
<212> DNA
<213> Homo sapiens

<400> 296
gggcggcggg atggggggccg ggggcggcgg gcgccgcact cgctgaggcc 50
ccgacgcagg gccggggccg gccacggggc gaggagcgcg gcggccagag 100
cgggggccgcg gaggcgacgc cggggacgcc cgcgcgacga gcaggtggcg 150
gcggtctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200
ggctctgctg accttgtgcc ttggacggct gtctcagcg agggggccgtg 250
caccgcctcc tgagcagcgc catgggcctg ctggccttcc tgaagaccca 300
gttcgtgctg cacctgctgg tcggctttgt cttcgtggtg agtggctctg 350
tcatcaactt cgtccagctg tgcacgctgg cgctctggcc ggtcagcaag 400
cagctctacc gccgcctcaa ctgccgcctc gcctactcac tctggagcca 450
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cggaccaggc cacggtagag cgctttggga aggagcacgc agtcatcatc 550
ctcaaccaca acttcgagat cgacttcctc tgtgggtgga ccatgtgtga 600
gcgcttcgga gtgctgggga gctccaaggc cctcgctaag aaggagctgc 650
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cttcaccacc gcagtcaagt gcctccgggg gacagtcgca gctgtctatg 950
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ctctacggga agaagtacga ggcggacatg tgcgtagga gatttcctct 1050
ggaagacatc ccgctggatg aaaaggaagc agctcagtgg cttcataaac 1100
tgtaccagga gaaggacgcg ctccaggaga tatataatca gaaggcatg 1150

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 aggaaaatta acagcctcag agacccatgg tgcaccgtca cacaatatca 1650
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 aatggccaca agctgatgaa aaacagtaac ctaccactc aggaagctca 1750
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 aatcaaagtg tcaaatgaca aagaatcttg aaagcagcaa gagatgagca 1850
 acttatcttg ttcaaaggat ctttgatcag attaacagct catttctcct 1900
 cagaaatcat gggagccagg agatagtggg atgaacactg ttgaaggcaa 1950
 aaccttcaac tgtaattatt ggacttttga gtcttagatg gtcctgacct 2000
 ctttgtcttc agggacagtt tttcaattta atccctaata acaattagtc 2050
 aagcttcctt gacctgtagg aaggcctgtc tttaggccgg gcacagtggc 2100
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 gcctccaaa gtgttgtgat tgcaggcgtg agccactgcg cctggccgga 2250
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 gtgatcccaa gtagcttga ttgtaaacaat gcaccacat gcctggctaa 2350
 tttttgtatt tttagtagag acgtgttagc caggctggtc tcgatctcct 2400
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 cgtgagccac tgtgcctggc cttgagcatc ttgtgatgtg cttattggcc 2500
 atttgtatat cttctatctt ctttggggaa atgtctgttc aagtcctttg 2550
 cctttttaaa tttttattat ttattttatt atttattttg agacagggtc 2600

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 catgagccac tgcacctggc aaactcccaa aattcaacac acacacacaa 2900
 aaaaccacct gattcaaaat gggcagaggg gccgggtgtg gcccctaacta 2950
 ccagggagac tgaagtggga ggatcgcttg ggcatgagaa gtcgaggctg 3000
 cagtgagtcg aggttgtgcg actgcattcc agcctggaca acagagtgag 3050
 accctgtctc 3060

<210> 297

<211> 368

<212> PRT

<213> Homo sapiens

<400> 297

Met	Gly	Leu	Leu	Ala	Phe	Leu	Lys	Thr	Gln	Phe	Val	Leu	His	Leu	1	5	10	15
Leu	Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	Phe	20	25	30	
Val	Gln	Leu	Cys	Thr	Leu	Ala	Leu	Trp	Pro	Val	Ser	Lys	Gln	Leu	35	40	45	
Tyr	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	Gln	50	55	60	
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Cys	Thr	Glu	Cys	Thr	Leu	65	70	75	
Phe	Thr	Asp	Gln	Ala	Thr	Val	Glu	Arg	Phe	Gly	Lys	Glu	His	Ala	80	85	90	
Val	Ile	Ile	Leu	Asn	His	Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly	95	100	105	
Trp	Thr	Met	Cys	Glu	Arg	Phe	Gly	Val	Leu	Gly	Ser	Ser	Lys	Val	110	115	120	
Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	Gly	Trp	Thr	125	130	135	
Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	Glu	140	145	150	
Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu	Arg	Arg	Leu	Ser	Asp	Tyr	155	160	165	

Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe	
				170					175					180	
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys	
				185					190					195	
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly	
				200					205					210	
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val	
				215					220					225	
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu	
				230					235					240	
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val	
				245					250					255	
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala	
				260					265					270	
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln	
				275					280					285	
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys	
				290					295					300	
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala	
				305					310					315	
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe	
				320					325					330	
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val	
				335					340					345	
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Glu	Ser	Leu	
				350					355					360	
Glu	Pro	Gly	Arg	Trp	Arg	Leu	Gln								
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<210> 298

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 298

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<210> 299

<211> 21

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299

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<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300

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<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

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cgcccttggg ttagaaggga agggaagata aacttttata caaatgggga 250
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ataccttctt ttctctaacc tggcataccc tgcttaaagc ctctcagggc 350
ttctctctgt tcttaggatc aaagtattta gagctacaag agccctcatg 400
gtctggcccc tgccccctg gccagettca ttgtacatgt ggtgttctct 450
tgtcgttcct gtaatgtggt atgcatggg gtctttgcac aagcctttcc 500
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atgtagtcat cctgcagatt tcaattctaa catcattttc tccagggatc 600
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ttcccttttg cagcacttgc cactcagttg tatctttatg tgcgtttgtg 700
gttgatatggg ttgtgtctgt tccccagaat gccagctct gagctgcgtg 750

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 ggtgctcatg ttttagagac taaatggagg aggagatgag gaaaagattg 850
 aaatctctca gttcaccaga tgggtgtaggg ccagcattg taaattcaca 900
 cggtgactgt gcttgtgaat tatctgggga tgcaggtcct gattcagtag 950
 gccaggttg ggcatctcta acaaactccc acgtgatgct gatgctggtc 1000
 ctatgaacta tactaaatag taagaatcta tggagccagg ctgggcatgg 1050
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 acctggagtc aggatttcaa gactagcctg gccaacatgg tggaacccca 1150
 tctgtactaa aaatacacia attagctggg catggtggca catgcctgta 1200
 gtcccagcta ctggggaggc tgaagcaaga gaatcgcttg aacctgggag 1250
 gcggaggttg cagtgagccg agatcaggcc actgtattcc aaccaggtg 1300
 acagagtgag actctatgtc caaaaaaaaa aaaa 1334

<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

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His	Leu	Cys	Val	Cys	Phe	Ser	Phe	Ala	Leu	Ala	Leu	Gly	His	Phe
				20					25					30
Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly
				35					40					45
Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val
				50					55					60
Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp
				65					70					75
Gly	Leu	Arg	Pro	Ala	Ser	Ser	Val	Lys	Phe	Leu	Gly	Ser	Ala	Tyr
				80					85					90
Thr	Phe	Phe	Ser	Leu	Thr	Trp	His	Thr	Leu	Leu	Lys	Ala	Ser	Gln
				95					100					105
Gly	Phe	Ser	Leu	Phe	Leu	Gly	Ser	Lys	Tyr	Leu	Glu	Leu	Gln	Glu
				110					115					120
Pro	Ser	Trp	Ser	Gly	Pro	Cys	Pro	Pro	Gly	Gln	Leu	His	Cys	Thr
				125					130					135
Cys	Gly	Val	Leu	Leu	Ser	Phe	Leu							

<210> 303

<211> 1768

<212> DNA

<213> Homo sapiens

<400> 303

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<210> 304

<211> 109

<212> PRT

<213> Homo sapiens

<400> 304

Met	Leu	Trp	Trp	Leu	Val	Leu	Leu	Leu	Leu	Pro	Thr	Leu	Lys	Ser
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Val	Phe	Cys	Ser	Leu	Val	Thr	Ser	Leu	Tyr	Leu	Pro	Asn	Thr	Glu
				20					25					30
Asp	Leu	Ser	Leu	Trp	Leu	Trp	Pro	Lys	Pro	Asp	Leu	His	Ser	Gly
				35					40					45
Thr	Arg	Thr	Glu	Val	Ser	Thr	His	Thr	Val	Pro	Ser	Lys	Pro	Gly
				50					55					60
Thr	Ala	Ser	Pro	Cys	Trp	Pro	Leu	Ala	Gly	Ala	Val	Pro	Ser	Pro
				65					70					75
Thr	Val	Ser	Arg	Leu	Glu	Ala	Leu	Thr	Arg	Ala	Val	Gln	Val	Ala
				80					85					90
Glu	Pro	Leu	Gly	Ser	Cys	Gly	Phe	Gln	Gly	Gly	Pro	Cys	Pro	Gly
				95					100					105
Arg	Arg	Arg	Asp											

<210> 305

<211> 989

<212> DNA

<213> Homo sapiens

<400> 305

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 ccgccttcgc cactggcctc ttctgggga ggcggtgcc cccatggcga 200
 ggccggcgag agcagtgcct gcttcccccc gaggacagcc gcctgtggca 250
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<210> 306

<211> 262

<212> PRT

<213> Homo sapiens

<400> 306

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Leu	Gly	Ser	Ala	Ala	Leu	Gly	Ala	Ala	Phe	Ala	Thr	Gly	Leu	Phe
			20						25					30
Leu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys
				35					40					45
Leu	Leu	Pro	Pro	Glu	Asp	Ser	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ser
				50					55					60

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 ggcagtggc ctgacgagga cgatgaggac cgggggggtca tggccgtcac 450
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<210> 308

<211> 671

<212> PRT

<213> Homo sapiens

<400> 308

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				20					25					30
Gly	Ala	Val	Lys	Pro	Pro	Pro	Asn	Lys	Tyr	Pro	Ile	Phe	Phe	Phe
				35					40					45
Gly	Thr	His	Glu	Thr	Ala	Phe	Leu	Gly	Pro	Lys	Asp	Leu	Phe	Pro
				50					55					60
Tyr	Asp	Lys	Cys	Lys	Asp	Lys	Tyr	Gly	Lys	Pro	Asn	Lys	Arg	Lys
				65					70					75
Gly	Phe	Asn	Glu	Gly	Leu	Trp	Glu	Ile	Gln	Asn	Asn	Pro	His	Ala
				80					85					90
Ser	Tyr	Ser	Ala	Pro	Pro	Pro	Val	Ser	Ser	Ser	Asp	Ser	Glu	Ala
				95					100					105
Pro	Glu	Ala	Asn	Pro	Ala	Asp	Gly	Ser	Asp	Ala	Asp	Glu	Asp	Asp
				110					115					120
Glu	Asp	Arg	Gly	Val	Met	Ala	Val	Thr	Ala	Val	Thr	Ala	Thr	Ala
				125					130					135
Ala	Ser	Asp	Arg	Met	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Lys	Ser	Ser

				140					145					150
Asp	Asn	Ser	Gly	Leu	Lys	Arg	Lys	Thr	Pro	Ala	Leu	Lys	Met	Ser
				155					160					165
Val	Ser	Lys	Arg	Ala	Arg	Lys	Ala	Ser	Ser	Asp	Leu	Asp	Gln	Ala
				170					175					180
Ser	Val	Ser	Pro	Ser	Glu	Glu	Glu	Asn	Ser	Glu	Ser	Ser	Ser	Glu
				185					190					195
Ser	Glu	Lys	Thr	Ser	Asp	Gln	Asp	Phe	Thr	Pro	Glu	Lys	Lys	Ala
				200					205					210
Ala	Val	Arg	Ala	Pro	Arg	Arg	Gly	Pro	Leu	Gly	Gly	Arg	Lys	Lys
				215					220					225
Lys	Lys	Ala	Pro	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Lys	Ala	Asp	Ser
				230					235					240
Asp	Gly	Ala	Lys	Pro	Glu	Pro	Val	Ala	Met	Ala	Arg	Ser	Ala	Ser
				245					250					255
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Asp	Ser	Asp	Val	Ser	Val
				260					265					270
Lys	Lys	Pro	Pro	Arg	Gly	Arg	Lys	Pro	Ala	Glu	Lys	Pro	Leu	Pro
				275					280					285
Lys	Pro	Arg	Gly	Arg	Lys	Pro	Lys	Pro	Glu	Arg	Pro	Pro	Ser	Ser
				290					295					300
Ser	Ser	Ser	Asp	Ser	Asp	Ser	Asp	Glu	Val	Asp	Arg	Ile	Ser	Glu
				305					310					315
Trp	Lys	Arg	Arg	Asp	Glu	Ala	Arg	Arg	Arg	Glu	Leu	Glu	Ala	Arg
				320					325					330
Arg	Arg	Arg	Glu	Gln	Glu	Glu	Glu	Leu	Arg	Arg	Leu	Arg	Glu	Gln
				335					340					345
Glu	Lys	Glu	Glu	Lys	Glu	Arg	Arg	Arg	Glu	Arg	Ala	Asp	Arg	Gly
				350					355					360
Glu	Ala	Glu	Arg	Gly	Ser	Gly	Gly	Ser	Ser	Gly	Asp	Glu	Leu	Arg
				365					370					375
Glu	Asp	Asp	Glu	Pro	Val	Lys	Lys	Arg	Gly	Arg	Lys	Gly	Arg	Gly
				380					385					390
Arg	Gly	Pro	Pro	Ser	Ser	Ser	Asp	Ser	Glu	Pro	Glu	Ala	Glu	Leu
				395					400					405
Glu	Arg	Glu	Ala	Lys	Lys	Ser	Ala	Lys	Lys	Pro	Gln	Ser	Ser	Ser
				410					415					420
Thr	Glu	Pro	Ala	Arg	Lys	Pro	Gly	Gln	Lys	Glu	Lys	Arg	Val	Arg
				425					430					435

Pro	Glu	Glu	Lys	Gln	Gln	Ala	Lys	Pro	Val	Lys	Val	Glu	Arg	Thr	
				440					445					450	
Arg	Lys	Arg	Ser	Glu	Gly	Phe	Ser	Met	Asp	Arg	Lys	Val	Glu	Lys	
				455					460					465	
Lys	Lys	Glu	Pro	Ser	Val	Glu	Glu	Lys	Leu	Gln	Lys	Leu	His	Ser	
				470					475					480	
Glu	Ile	Lys	Phe	Ala	Leu	Lys	Val	Asp	Ser	Pro	Asp	Val	Lys	Arg	
				485					490					495	
Cys	Leu	Asn	Ala	Leu	Glu	Glu	Leu	Gly	Thr	Leu	Gln	Val	Thr	Ser	
				500					505					510	
Gln	Ile	Leu	Gln	Lys	Asn	Thr	Asp	Val	Val	Ala	Thr	Leu	Lys	Lys	
				515					520					525	
Ile	Arg	Arg	Tyr	Lys	Ala	Asn	Lys	Asp	Val	Met	Glu	Lys	Ala	Ala	
				530					535					540	
Glu	Val	Tyr	Thr	Arg	Leu	Lys	Ser	Arg	Val	Leu	Gly	Pro	Lys	Ile	
				545					550					555	
Glu	Ala	Val	Gln	Lys	Val	Asn	Lys	Ala	Gly	Met	Glu	Lys	Glu	Lys	
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Ala	Glu	Glu	Lys	Leu	Ala	Gly	Glu	Glu	Leu	Ala	Gly	Glu	Glu	Ala	
				575					580					585	
Pro	Gln	Glu	Lys	Ala	Glu	Asp	Lys	Pro	Ser	Thr	Asp	Leu	Ser	Ala	
				590					595					600	
Pro	Val	Asn	Gly	Glu	Ala	Thr	Ser	Gln	Lys	Gly	Glu	Ser	Ala	Glu	
				605					610					615	
Asp	Lys	Glu	His	Glu	Glu	Gly	Arg	Asp	Ser	Glu	Glu	Gly	Pro	Arg	
				620					625					630	
Cys	Gly	Ser	Ser	Glu	Asp	Leu	His	Asp	Ser	Val	Arg	Glu	Gly	Pro	
				635					640					645	
Asp	Leu	Asp	Arg	Pro	Gly	Ser	Asp	Arg	Gln	Glu	Arg	Glu	Arg	Ala	
				650					655					660	
Arg	Gly	Asp	Ser	Glu	Ala	Leu	Asp	Glu	Glu	Ser					
				665					670						

<210> 309
 <211> 3871
 <212> DNA
 <213> Homo sapiens

<400> 309
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 ttttcacctt tttcctgctt tgatgatgct aagcatgacc atgttggttc 200
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 tcagagtact tcagccctat aacaaaactc acatatatgt gtgtggaact 550
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<210> 310
 <211> 777
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Lys Leu Thr Tyr Lys Asp Leu Leu Leu Ser Asn Ser Cys Ile Pro
 50 55 60
 Phe Leu Gly Ser Ser Glu Gly Leu Asp Phe Gln Thr Leu Leu Leu
 65 70 75
 Asp Glu Glu Arg Gly Arg Leu Leu Leu Gly Ala Lys Asp His Ile

	80	85	90
Phe Leu Leu Ser	Leu Val Asp Leu Asn	Lys Asn Phe Lys Lys	Ile 105
	95	100	
Tyr Trp Pro Ala	Ala Lys Glu Arg Val	Glu Leu Cys Lys Leu	Ala 120
	110	115	
Gly Lys Asp Ala	Asn Thr Glu Cys Ala	Asn Phe Ile Arg Val	Leu 135
	125	130	
Gln Pro Tyr Asn	Lys Thr His Ile Tyr	Val Cys Gly Thr Gly	Ala 150
	140	145	
Phe His Pro Ile	Cys Gly Tyr Ile Asp	Leu Gly Val Tyr Lys	Glu 165
	155	160	
Asp Ile Ile Phe	Lys Leu Asp Thr His	Asn Leu Glu Ser Gly	Arg 180
	170	175	
Leu Lys Cys Pro	Phe Asp Pro Gln Gln	Pro Phe Ala Ser Val	Met 195
	185	190	
Thr Asp Glu Tyr	Leu Tyr Ser Gly Thr	Ala Ser Asp Phe Leu	Gly 210
	200	205	
Lys Asp Thr Ala	Phe Thr Arg Ser Leu	Gly Pro Thr His Asp	His 225
	215	220	
His Tyr Ile Arg	Thr Asp Ile Ser Glu	His Tyr Trp Leu Asn	Gly 240
	230	235	
Ala Lys Phe Ile	Gly Thr Phe Phe Ile	Pro Asp Thr Tyr Asn	Pro 255
	245	250	
Asp Asp Asp Lys	Ile Tyr Phe Phe Phe	Arg Glu Ser Ser Gln	Glu 270
	260	265	
Gly Ser Thr Ser	Asp Lys Thr Ile Leu	Ser Arg Val Gly Arg	Val 285
	275	280	
Cys Lys Asn Asp	Val Gly Gly Gln Arg	Ser Leu Ile Asn Lys	Trp 300
	290	295	
Thr Thr Phe Leu	Lys Ala Arg Leu Ile	Cys Ser Ile Pro Gly	Ser 315
	305	310	
Asp Gly Ala Asp	Thr Tyr Phe Asp Glu	Leu Gln Asp Ile Tyr	Leu 330
	320	325	
Leu Pro Thr Arg	Asp Glu Arg Asn Pro	Val Val Tyr Gly Val	Phe 345
	335	340	
Thr Thr Thr Ser	Ser Ile Phe Lys Gly	Ser Ala Val Cys Val	Tyr 360
	350	355	
Ser Met Ala Asp	Ile Arg Ala Val Phe	Asn Gly Pro Tyr Ala	His 375
	365	370	

Lys	Glu	Ser	Ala	Asp	His	Arg	Trp	Val	Gln	Tyr	Asp	Gly	Arg	Ile	380	385	390
Pro	Tyr	Pro	Arg	Pro	Gly	Thr	Cys	Pro	Ser	Lys	Thr	Tyr	Asp	Pro	395	400	405
Leu	Ile	Lys	Ser	Thr	Arg	Asp	Phe	Pro	Asp	Asp	Val	Ile	Ser	Phe	410	415	420
Ile	Lys	Arg	His	Ser	Val	Met	Tyr	Lys	Ser	Val	Tyr	Pro	Val	Ala	425	430	435
Gly	Gly	Pro	Thr	Phe	Lys	Arg	Ile	Asn	Val	Asp	Tyr	Arg	Leu	Thr	440	445	450
Gln	Ile	Val	Val	Asp	His	Val	Ile	Ala	Glu	Asp	Gly	Gln	Tyr	Asp	455	460	465
Val	Met	Phe	Leu	Gly	Thr	Asp	Ile	Gly	Thr	Val	Leu	Lys	Val	Val	470	475	480
Ser	Ile	Ser	Lys	Glu	Lys	Trp	Asn	Met	Glu	Glu	Val	Val	Leu	Glu	485	490	495
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Arg	Arg	Gln	Asp	Val	Lys	Tyr	Gly	Asp	Pro	Ile	Thr	Gln	Cys	Trp	575	580	585
Asp	Ile	Glu	Asp	Ser	Ile	Ser	His	Glu	Thr	Ala	Asp	Glu	Lys	Val	590	595	600
Ile	Phe	Gly	Ile	Glu	Phe	Asn	Ser	Thr	Phe	Leu	Glu	Cys	Ile	Pro	605	610	615
Lys	Ser	Gln	Gln	Ala	Thr	Ile	Lys	Trp	Tyr	Ile	Gln	Arg	Ser	Gly	620	625	630
Asp	Glu	His	Arg	Glu	Glu	Leu	Lys	Pro	Asp	Glu	Arg	Ile	Ile	Lys	635	640	645
Thr	Glu	Tyr	Gly	Leu	Leu	Ile	Arg	Ser	Leu	Gln	Lys	Lys	Asp	Ser	650	655	660
Gly	Met	Tyr	Tyr	Cys	Lys	Ala	Gln	Glu	His	Thr	Phe	Ile	His	Thr			

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Ile Val Lys Leu Thr Leu Asn Val Ile Glu Asn Glu Gln Met Glu					
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Asn Thr Gln Arg Ala Glu His Glu Glu Gly Gln Val Lys Asp Leu					
	695		700		705
Leu Ala Glu Ser Arg Leu Arg Tyr Lys Asp Tyr Ile Gln Ile Leu					
	710		715		720
Ser Ser Pro Asn Phe Ser Leu Asp Gln Tyr Cys Glu Gln Met Trp					
	725		730		735
His Arg Glu Lys Arg Arg Gln Arg Asn Lys Gly Gly Pro Lys Trp					
	740		745		750
Lys His Met Gln Glu Met Lys Lys Lys Arg Asn Arg Arg His His					
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Arg Asp Leu Asp Glu Leu Pro Arg Ala Val Ala Thr					
	770		775		

<210> 311
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 <213> Artificial

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 <223> Synthetic construct.

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<210> 312
 <211> 24
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-24
 <223> Synthetic construct.

<400> 312
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<210> 313
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 313
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<210> 314
<211> 3934
<212> DNA
<213> Homo sapiens

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<210> 315

<211> 370

<212> PRT

<213> Homo sapiens

<400> 315

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Val	Phe	Pro	Pro	Thr	Pro	Val	Leu	Cys	Leu	Pro	Asn	Gln	Val	Leu	
				20					25					30	
Gln	Arg	Leu	Glu	Gln	Arg	Arg	Gln	Gln	Ala	Ser	Glu	Arg	Glu	Ala	
				35					40					45	
Pro	Ser	Ile	Glu	Gln	Arg	Leu	Gln	Glu	Val	Arg	Glu	Ser	Ile	Arg	
				50					55					60	
Arg	Ala	Gln	Val	Ser	Gln	Val	Lys	Gly	Ala	Ala	Arg	Leu	Ala	Leu	
				65					70					75	
Leu	Gln	Gly	Ala	Gly	Leu	Asp	Val	Glu	Arg	Trp	Leu	Lys	Pro	Ala	
				80					85					90	
Met	Thr	Gln	Ala	Gln	Asp	Glu	Val	Glu	Gln	Glu	Arg	Arg	Leu	Ser	
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Glu	Ala	Arg	Leu	Ser	Gln	Arg	Asp	Leu	Ser	Pro	Thr	Ala	Glu	Asp	
				110					115					120	
Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu	
				125					130					135	
Phe	Glu	Glu	Pro	Ala	Pro	Gln	Ala	Leu	Ala	Thr	Arg	Ala	Leu	Pro	
				140					145					150	
Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp	
				155					160					165	
Glu	Leu	Thr	Ile	Thr	Glu	Gly	Glu	Trp	Leu	Glu	Val	Ile	Glu	Glu	
				170					175					180	
Gly	Asp	Ala	Asp	Glu	Trp	Val	Lys	Ala	Arg	Asn	Gln	His	Gly	Glu	
				185					190					195	
Val	Gly	Phe	Val	Pro	Glu	Arg	Tyr	Leu	Asn	Phe	Pro	Asp	Leu	Ser	
				200					205					210	
Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu	
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Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln	
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Ser	Ala	Glu	Glu	Leu	Ser	Phe	Pro	Glu	Gly	Ala	Leu	Ile	Arg	Leu	
				245					250					255	
Leu	Pro	Arg	Ala	Gln	Asp	Gly	Val	Asp	Asp	Gly	Phe	Trp	Arg	Gly	
				260					265					270	
Glu	Phe	Gly	Gly	Arg	Val	Gly	Val	Phe	Pro	Ser	Leu	Leu	Val	Glu	
				275					280					285	
Glu	Leu	Leu	Gly	Pro	Pro	Gly	Pro	Pro	Glu	Leu	Ser	Asp	Pro	Glu	
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Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala	

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ccaataataa tacctccctt agaagtttgt tgtgaggatt aaataatgta 4300
aataaagaac tagcataaca ctcaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4350
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aaggaaa 4407

<210> 317
<211> 837
<212> PRT
<213> Homo sapiens

<400> 317
Met Ser Gln Thr Gly Ser His Pro Gly Arg Gly Leu Ala Gly Arg
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Trp Leu Trp Gly Ala Gln Pro Cys Leu Leu Leu Pro Ile Val Pro
20 25 30
Leu Ser Trp Leu Val Trp Leu Leu Leu Leu Leu Ala Ser Leu
35 40 45
Leu Pro Ser Ala Arg Leu Ala Ser Pro Leu Pro Arg Glu Glu Glu
50 55 60
Ile Val Phe Pro Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser
65 70 75
Gly Ala Pro Ala Arg Leu Leu Cys Arg Leu Gln Ala Phe Gly Glu
80 85 90
Thr Leu Leu Leu Glu Leu Glu Gln Asp Ser Gly Val Gln Val Glu
95 100 105
Gly Leu Thr Val Gln Tyr Leu Gly Gln Ala Pro Glu Leu Leu Gly
110 115 120
Gly Ala Glu Pro Gly Thr Tyr Leu Thr Gly Thr Ile Asn Gly Asp
125 130 135
Pro Glu Ser Val Ala Ser Leu His Trp Asp Gly Gly Ala Leu Leu

				140					145					150
Gly	Val	Leu	Gln	Tyr 155	Arg	Gly	Ala	Glu	Leu 160	His	Leu	Gln	Pro	Leu 165
Glu	Gly	Gly	Thr	Pro 170	Asn	Ser	Ala	Gly	Gly 175	Pro	Gly	Ala	His	Ile 180
Leu	Arg	Arg	Lys	Ser 185	Pro	Ala	Ser	Gly	Gln 190	Gly	Pro	Met	Cys	Asn 195
Val	Lys	Ala	Pro	Leu 200	Gly	Ser	Pro	Ser	Pro 205	Arg	Pro	Arg	Arg	Ala 210
Lys	Arg	Phe	Ala	Ser 215	Leu	Ser	Arg	Phe	Val 220	Glu	Thr	Leu	Val	Val 225
Ala	Asp	Asp	Lys	Met 230	Ala	Ala	Phe	His	Gly 235	Ala	Gly	Leu	Lys	Arg 240
Tyr	Leu	Leu	Thr	Val 245	Met	Ala	Ala	Ala	Ala 250	Lys	Ala	Phe	Lys	His 255
Pro	Ser	Ile	Arg	Asn 260	Pro	Val	Ser	Leu	Val 265	Val	Thr	Arg	Leu	Val 270
Ile	Leu	Gly	Ser	Gly 275	Glu	Glu	Gly	Pro	Gln 280	Val	Gly	Pro	Ser	Ala 285
Ala	Gln	Thr	Leu	Arg 290	Ser	Phe	Cys	Ala	Trp 295	Gln	Arg	Gly	Leu	Asn 300
Thr	Pro	Glu	Asp	Ser 305	Gly	Pro	Asp	His	Phe 310	Asp	Thr	Ala	Ile	Leu 315
Phe	Thr	Arg	Gln	Asp 320	Leu	Cys	Gly	Val	Ser 325	Thr	Cys	Asp	Thr	Leu 330
Gly	Met	Ala	Asp	Val 335	Gly	Thr	Val	Cys	Asp 340	Pro	Ala	Arg	Ser	Cys 345
Ala	Ile	Val	Glu	Asp 350	Asp	Gly	Leu	Gln	Ser 355	Ala	Phe	Thr	Ala	Ala 360
His	Glu	Leu	Gly	His 365	Val	Phe	Asn	Met	Leu 370	His	Asp	Asn	Ser	Lys 375
Pro	Cys	Ile	Ser	Leu 380	Asn	Gly	Pro	Leu	Ser 385	Thr	Ser	Arg	His	Val 390
Met	Ala	Pro	Val	Met 395	Ala	His	Val	Asp	Pro 400	Glu	Glu	Pro	Trp	Ser 405
Pro	Cys	Ser	Ala	Arg 410	Phe	Ile	Thr	Asp	Phe 415	Leu	Asp	Asn	Gly	Tyr 420
Gly	His	Cys	Leu	Leu 425	Asp	Lys	Pro	Glu	Ala 430	Pro	Leu	His	Leu	Pro 435

Val Thr Phe Pro Gly Lys Asp Tyr Asp	Ala Asp Arg Gln Cys Gln	440	445	450
Leu Thr Phe Gly Pro Asp Ser Arg His	Cys Pro Gln Leu Pro Pro	455	460	465
Pro Cys Ala Ala Leu Trp Cys Ser Gly	His Leu Asn Gly His Ala	470	475	480
Met Cys Gln Thr Lys His Ser Pro Trp	Ala Asp Gly Thr Pro Cys	485	490	495
Gly Pro Ala Gln Ala Cys Met Gly Gly	Arg Cys Leu His Met Asp	500	505	510
Gln Leu Gln Asp Phe Asn Ile Pro Gln	Ala Gly Gly Trp Gly Pro	515	520	525
Trp Gly Pro Trp Gly Asp Cys Ser Arg	Thr Cys Gly Gly Gly Val	530	535	540
Gln Phe Ser Ser Arg Asp Cys Thr Arg	Pro Val Pro Arg Asn Gly	545	550	555
Gly Lys Tyr Cys Glu Gly Arg Arg Thr	Arg Phe Arg Ser Cys Asn	560	565	570
Thr Glu Asp Cys Pro Thr Gly Ser Ala	Leu Thr Phe Arg Glu Glu	575	580	585
Gln Cys Ala Ala Tyr Asn His Arg Thr	Asp Leu Phe Lys Ser Phe	590	595	600
Pro Gly Pro Met Asp Trp Val Pro Arg	Tyr Thr Gly Val Ala Pro	605	610	615
Gln Asp Gln Cys Lys Leu Thr Cys Gln	Ala Arg Ala Leu Gly Tyr	620	625	630
Tyr Tyr Val Leu Glu Pro Arg Val Val	Asp Gly Thr Pro Cys Ser	635	640	645
Pro Asp Ser Ser Ser Val Cys Val Gln	Gly Arg Cys Ile His Ala	650	655	660
Gly Cys Asp Arg Ile Ile Gly Ser Lys	Lys Lys Phe Asp Lys Cys	665	670	675
Met Val Cys Gly Gly Asp Gly Ser Gly	Cys Ser Lys Gln Ser Gly	680	685	690
Ser Phe Arg Lys Phe Arg Tyr Gly Tyr	Asn Asn Val Val Thr Ile	695	700	705
Pro Ala Gly Ala Thr His Ile Leu Val	Arg Gln Gln Gly Asn Pro	710	715	720
Gly His Arg Ser Ile Tyr Leu Ala Leu	Lys Leu Pro Asp Gly Ser			

	725		730		735									
Tyr	Ala	Leu	Asn	Gly	Glu	Tyr	Thr	Leu	Met	Pro	Ser	Pro	Thr	Asp
				740					745					750
Val	Val	Leu	Pro	Gly	Ala	Val	Ser	Leu	Arg	Tyr	Ser	Gly	Ala	Thr
				755					760					765
Ala	Ala	Ser	Glu	Thr	Leu	Ser	Gly	His	Gly	Pro	Leu	Ala	Gln	Pro
				770					775					780
Leu	Thr	Leu	Gln	Val	Leu	Val	Ala	Gly	Asn	Pro	Gln	Asp	Thr	Arg
				785					790					795
Leu	Arg	Tyr	Ser	Phe	Phe	Val	Pro	Arg	Pro	Thr	Pro	Ser	Thr	Pro
				800					805					810
Arg	Pro	Thr	Pro	Gln	Asp	Trp	Leu	His	Arg	Arg	Ala	Gln	Ile	Leu
				815					820					825
Glu	Ile	Leu	Arg	Arg	Arg	Pro	Trp	Ala	Gly	Arg	Lys			
				830					835					

<210> 318
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 318
 ccctgaagct gccagatggc tcc 23

<210> 319
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 319
 ctgtgctctt cggtgcagcc agtc 24

<210> 320
 <211> 43
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-43
 <223> Synthetic construct.

<400> 320
ccacagatgt ggtactgcct ggggcagtca gcttgcgcta cag 43

<210> 321
<211> 1197
<212> DNA
<213> Homo sapiens

<400> 321
cagcagtggg ctctcagtc tctcaaagca aggaaagagt actgtgtgct 50
gagagaccat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt 100
ctaaatgcag aagcttttaa atccaagaaa atatgtaaat cacttaagat 150
ttgtggactg gtgtttggta tcttggccct aactctaatt gtctgtttt 200
gggggagcaa gcacttctgg ccggagggtac ccaaaaaagc ctatgacatg 250
gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300
tgatcctgtg accagaactg aaatattcag aagcggaaat ggcaactgatg 350
aaacattgga agtgcacgac tttaaaaacg gatacactgg catctacttc 400
gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450
attttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500
ctttctttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550
aaccgagatt ttcttaaaaa ttccaaaatt ctggagattt gtgataacgt 600
gaccatgtat tggatcaatc ccaacttaat atcagtttct gagttacaag 650
actttgagga ggaggagaa gatcttact ttcctgcaa cgaaaaaaaa 700
gggattgaac aaaatgaaca gtgggtggc cctcaagtga aagtagagaa 750
gaccgcgtcac gccagacaag caagtgagga agaacttcca ataatgact 800
atactgaaaa tggaatagaa tttgatccca tgctggatga gagaggttat 850
tgttgtatct actgccgtcg aggcaaccgc tattgccgcc gcgtctgtga 900
acctttacta ggctactacc catatccata ctgctaccaa ggaggacgag 950
tcatctgtcg tgtcatcatg ccttgtaact ggtgggtggc ccgcatgctg 1000
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cccctggtag ccagctctcc agaattactt gtaggtaatt cctctcttca 1150
tggttctaata aacttctaca ttatcaccaa aaaaaaaaaa aaaaaa 1197

<210> 322

<211> 317
 <212> PRT
 <213> Homo sapiens

<400> 322

Met	Ala	Lys	Asn	Pro	Pro	Glu	Asn	Cys	Glu	Asp	Cys	His	Ile	Leu	
1				5					10					15	
Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys	
				20					25					30	
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val	
				35					40					45	
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys	
				50					55					60	
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys	
				65					70					75	
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe	
				80					85					90	
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe	
				95					100					105	
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys	
				110					115					120	
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro	
				125					130					135	
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe	
				140					145					150	
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn	
				155					160					165	
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn	
				170					175					180	
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu	
				185					190					195	
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala	
				200					205					210	
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro	
				215					220					225	
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu	
				230					235					240	
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe	
				245					250					255	
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg	
				260					265					270	

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly
275 280 285

Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
290 295 300

Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly
305 310 315

Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

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ggccgtgcag cttctgggct tcctgctcag cttcctgggc atggtgggca 150
cgttgatcac caccatcctg ccgcactggc ggaggacagc gcacgtgggc 200
accaacatcc tcacggccgt gtcctacctg aaagggctct ggatggagtg 250
tgtgtggcac agcacaggca tctaccagtg ccagatctac cgatccctgc 300
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 gtttggtcag tggggttggt ttgtgatcca ggaataaacc ttgcggatgt 1150
 ggctgtttat gaaaaaaaaa aaaa 1174

<210> 324
 <211> 239
 <212> PRT
 <213> Homo sapiens

<400> 324
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 Leu Gly Met Val Gly Thr Leu Ile Thr Thr Ile Leu Pro His Trp
 20 25 30
 Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser
 35 40 45
 Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly
 50 55 60
 Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln
 65 70 75
 Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu
 80 85 90
 Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr
 95 100 105
 Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu
 110 115 120
 Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala
 125 130 135
 Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro
 140 145 150
 Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr
 155 160 165
 Leu Gly Phe Ile Ser Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu
 170 175 180
 Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln
 185 190 195
 Ala Pro Pro Arg Ala Thr Thr Thr Thr Ala Asn Thr Ala Pro Ala
 200 205 210
 Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val
 215 220 225

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val
 230 235

<210> 325
 <211> 2121
 <212> DNA
 <213> Homo sapiens

<400> 325
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 gcatcgcggc caccgggatg gacatgtgga gcaccagga cctgtacgac 200
 aaccccgctca cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt 250
 gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg 300
 gacttccagc catgctgcag gcagtgcgag ccctgatgat cgtaggcac 350
 gtcctgggtg ccattggcct cctggtatcc atctttgcc tgaaatgcat 400
 ccgcattggc agcatggagg actctgccaa agccaacatg aactgacct 450
 ccgggatcat gttcattgtc tcaggctctt gtgcaattgc tggagtgtct 500
 gtgtttgcc aatgctggt gactaacttc tggatgtcca cagctaacat 550
 gtacaccggc atgggtggga tgggtgcagac tgttcagacc aggtacacat 600
 ttggtgcggc tctgttcgtg ggctgggtcg ctggaggcct cacactaatt 650
 gggggtgtga tgatgtgcat cgctgccgg ggctggcac cagaagaaac 700
 caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca 750
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 aagaagatat acgatggagg tgccgcaca gaggacgagg tacaatctta 850
 tccttccaag cagactatg tgtaatgctc taagacctct cagcacgggc 900
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 cacttactga agaagaagca ataagagaaa gatatttgta atctctccag 1400
 cccatgatct cggtttttctt acactgtgat cttaaaagtt accaaaccaa 1450
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 tcttattaca gcaacacccat tctaggagtt tcctgagctc tccactggag 1550
 tcctctttct gtcgcgggtc agaaattgtc cctagatgaa tgagaaaatt 1600
 atttttttta atttaagtcc taaatatagt taaaataaat aatgttttag 1650
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 gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt 1750
 aaagtcatgc ttaagtacaa attccatgaa aagctcacac ctgtaatcct 1800
 agcactttgg gaggctgagg aggaaggatc acttgagccc agaagttcga 1850
 gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag 1900
 aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg 1950
 gaggctgagg tgggaggatc acttgagccc agggagggtt gggctgcagt 2000
 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050
 gtctaaaaaa ataaaaaata aataatggaa cacagcaagt cctaggaagt 2100
 aggttaaaac taattcttta a 2121

<210> 326
 <211> 261
 <212> PRT
 <213> Homo sapiens

<400> 326
 Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile
 1 5 10 15
 Leu Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp
 20 25 30
 Ser Thr Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln
 35 40 45
 Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe
 50 55 60
 Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met
 65 70 75
 Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly

tgctgcttcc gtgatgtcct tcttggtttt catgatggcc atccttggca 400
 tgaaatgcac caggtgcacg ggggacaatg agaaggtgaa ggctcacatt 450
 ctgctgacgg ctggaatcat cttcatcatc acgggcatgg tgggtgctcat 500
 ccoctgtgagc tgggttgcca atgccatcat cagagatttc tataactcaa 550
 tagtgaatgt tgcccaaaaa cgtgagcttg gagaagctct ctacttagga 600
 tggaccacgg cactggtgct gattgttgga ggagctctgt tctgctgctg 650
 tttttgttgc aacgaaaaga gcagtagcta cagatactcg ataccttccc 700
 atcgcacaa ccaaaaaagt tatcacaccg gaaagaagtc accgagcgtc 750
 tactccagaa gtcagtatgt gtagttgtgt atgttttttt aactttacta 800
 taaagccatg caaatgacaa aaatctatat tactttctca aaatggaccc 850
 caaagaaact ttgatttact gttcttaact gctaatctt aattacagga 900
 actgtgcatc agctatttat gattctataa gctatttcag cagaatgaga 950
 tattaaaccc aatgctttga ttgttctaga aagtatagta atttgttttc 1000
 taaggtggtt caagcatcta ctctttttat catttacttc aaaatgacat 1050
 tgctaaagac tgcattatth tactactgta atttctccac gacatagcat 1100
 tatgtacata gatgagtgta acatttatat ctcacataga gacatgctta 1150
 tatggtttta tttaaaatga aatgccagtc cattacactg aataaataga 1200
 actcaactat tgcttttcag ggaaatcatg gataggggtg aagaaggtta 1250
 ctattaattg tttaaaaaca gcttagggat taatgtctc catttataat 1300
 gaagattaaa atgaaggctt taatcagcat tgtaaaggaa attgaatggc 1350
 tttctgatat gctgtttttt agcctaggag ttagaaatcc taacttcttt 1400
 atcctcttct cccagaggct ttttttttct tgtgtattaa attaacattt 1450
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 agggctatac tcagaagaaa gataaaagtg tgatctaaga aaaagtgatg 1550
 gtttttaggaa agtgaaaata tttttgtttt tgtatttgaa gaagaatgat 1600
 gcattttgac aagaaatcat atatgtatgg atatatttta ataagtattt 1650
 gagtacagac tttgaggttt catcaatata aataaaagag cagaaaaata 1700
 tgtcttggtt ttcatttgct taccaaaaaa acaacaaca aaaaagttgt 1750
 cctttgagaa cttcacctgc tcctatgtgg gtacctgagt caaaattgtc 1800

atttttggttc tgtgaaaaat aaatttcctt ctgtaccat ttctgttttag 1850
 ttttactaaa atctgtaaat actgtatttt tctgtttatt ccaaatttga 1900
 tgaaactgac aatccaattt gaaagtttgt gtcgacgtct gtctagctta 1950
 aatgaatgtg ttctatttgc tttatacatt tatattaata aattgtacat 2000
 tttttctaatt 2010

<210> 328
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 328
 Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly
 1 5 10 15
 Val Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp
 20 25 30
 Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn
 35 40 45
 Phe Trp Glu Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile
 50 55 60
 Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro
 65 70 75
 Asp Leu Gln Ala Ala Arg Gly Leu Met Cys Ala Ala Ser Val Met
 80 85 90
 Ser Phe Leu Ala Phe Met Met Ala Ile Leu Gly Met Lys Cys Thr
 95 100 105
 Arg Cys Thr Gly Asp Asn Glu Lys Val Lys Ala His Ile Leu Leu
 110 115 120
 Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met Val Val Leu Ile
 125 130 135
 Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp Phe Tyr Asn
 140 145 150
 Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly Glu Ala Leu
 155 160 165
 Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly Gly Ala
 170 175 180
 Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser Tyr
 185 190 195
 Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His
 200 205 210

Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val
				215				220						225

<210> 329
 <211> 1315
 <212> DNA
 <213> Homo sapiens

<400> 329
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 gaccgctttc atcggcaaca gcatcgtggt ggcccagggt gtgtgggagg 150
 gcctgtggat gtctgcgtg gtgcagagca ccggccagat gcagtgaag 200
 gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250
 cctctgtgtc atcgccctcc ttgtggccct gttcggcttg ctggtctacc 300
 ttgctggggc caagtgtacc acctgtgtgg aggagaagga ttccaaggcc 350
 cgctggtgc tcacctctgg gattgtcttt gtcattctcag gggctctgac 400
 gctaattccc gtgtgctgga cggcgcatgc catcatccgg gacttctata 450
 accccctggg ggctgaggcc caaaagcggg agctgggggc ctccctctac 500
 ttgggctggg cggcctcagg ccttttgttg ctgggtgggg ggttgctgtg 550
 ctgcacttgc ccctcggggg ggtcccaggg cccagccat tacatggccc 600
 gctactcaac atctgccct gccatctctc gggggccctc tgagtaccct 650
 accaagaatt acgtctgacg tggaggggaa tgggggctcc gctggcgcta 700
 gagccatcca gaagtggcag tgcccaacag ctttgggatg ggttcgtacc 750
 ttttgtttct gcctcctgct atttttcttt tgactgagga tatttaaaat 800
 tcatttgaaa actgagccaa ggtgttgact cagactctca cttaggctct 850
 gctgtttctc acccttggat gatggagcca aagaggggat gctttgagat 900
 tctggatctt gacatgccca tcttagaagc cagtcaagct atggaactaa 950
 tgcggaggct gcttgctgtg ctggctttgc aacaagacag actgtcccca 1000
 agagttcctg ctgctgctgg gggctgggct tccctagatg tcaactggaca 1050
 gctgcccccc atcctactca ggtctctgga gctcctctct tcacccctgg 1100
 aaaaacaaat catctgttaa caaaggactg cccacctccg gaacttctga 1150
 cctctgtttc ctccgtcctg ataagacgtc cccccccag ggccagggtcc 1200
 cagctatgta gacccccgcc cccacctcca aactgcacc cttctgcct 1250

gccccctcg tctcaccccc ttacactca catttttatc aaataaagca 1300
 tgttttgtta gtgca 1315

<210> 330
 <211> 220
 <212> PRT
 <213> Homo sapiens

<400> 330
 Met Ala Ser Ala Gly Met Gln Ile Leu Gly Val Val Leu Thr Leu
 1 5 10 15
 Leu Gly Trp Val Asn Gly Leu Val Ser Cys Ala Leu Pro Met Trp
 20 25 30
 Lys Val Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val
 35 40 45
 Val Trp Glu Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly
 50 55 60
 Gln Met Gln Cys Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln
 65 70 75
 Asp Leu Gln Ala Ala Arg Ala Leu Cys Val Ile Ala Leu Leu Val
 80 85 90
 Ala Leu Phe Gly Leu Leu Val Tyr Leu Ala Gly Ala Lys Cys Thr
 95 100 105
 Thr Cys Val Glu Glu Lys Asp Ser Lys Ala Arg Leu Val Leu Thr
 110 115 120
 Ser Gly Ile Val Phe Val Ile Ser Gly Val Leu Thr Leu Ile Pro
 125 130 135
 Val Cys Trp Thr Ala His Ala Ile Ile Arg Asp Phe Tyr Asn Pro
 140 145 150
 Leu Val Ala Glu Ala Gln Lys Arg Glu Leu Gly Ala Ser Leu Tyr
 155 160 165
 Leu Gly Trp Ala Ala Ser Gly Leu Leu Leu Leu Gly Gly Gly Leu
 170 175 180
 Leu Cys Cys Thr Cys Pro Ser Gly Gly Ser Gln Gly Pro Ser His
 185 190 195
 Tyr Met Ala Arg Tyr Ser Thr Ser Ala Pro Ala Ile Ser Arg Gly
 200 205 210
 Pro Ser Glu Tyr Pro Thr Lys Asn Tyr Val
 215 220

<210> 331
 <211> 1160
 <212> DNA

<213> Homo sapiens

<400> 331

gccaaggaga acatcatcaa agacttctct agactcaaaa ggcttccacg 50
ttctacatct tgagcatctt ctaccactcc gaattgaacc agtcttcaaa 100
gtaaaggcaa tggcatttta tcccttgcaa attgctgggc tggttcttgg 150
gttccttggc atggtgggga ctcttgccac aacccttctg cctcagtgg 200
ggagtatcag cttttgttgg cagcaacatt attgtctttg agaggctctg 250
ggaagggctc tggatgaatt gcatccgaca agccagggtc cggttgcaat 300
gcaagttcta tagctccttg ttggctctcc cgctgacct ggaaacagcc 350
cgggccctca tgtgtgtggc tgttgctctc tccttgatcg ccctgcttat 400
tggcatctgt ggcatgaagc aggtccagtg cacaggctct aacgagagg 450
ccaaagcata ccttctggga acttcaggag tcctcttcat cctgacgggt 500
atcttcgttc tgattccggt gagctggaca gccaatataa tcatcagaga 550
tttctacaac ccagccatcc acataggta gaaacgagag ctgggagcag 600
cacttttcct tggctgggca agcgtgctg tcctcttcat tggaggggg 650
ctgctttgtg gattttgctg ctgcaacaga aagaagcaag ggtacagata 700
tccagtgcct ggctaccgtg tgccacacac agataagcga agaaatacga 750
caatgcttag taagacctcc accagttatg tctaatacct ccttttggct 800
ccaagtatgg actatggtca atgtttttta taaagtctg ctagaaactg 850
taagtatgtg aggcaggaga acttgcttta tgtctagatt tacattgata 900
cgaaagtttc aatttgttac tggtggtagg aatgaaaatg acttacttgg 950
acattctgac ttcaggtgta ttaaatgcat tgactattgt tggacccaat 1000
cgctgctcca attttcatat tctaaattca agtataccca taatcattag 1050
caagtgtaca atgatggact acttattact ttttgaccat catgtattat 1100
ctgataagaa tctaaagttg aaattgatat tctataacaa taaaacatat 1150
acctattcta 1160

<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met Asn Cys Ile Arg Gln Ala Arg Val Arg Leu Gln Cys Lys Phe

1	5	10	15
Tyr Ser Ser Leu Leu Ala Leu Pro Pro Ala Leu Glu Thr Ala Arg	20	25	30
Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu	35	40	45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn	50	55	60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe	65	70	75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala	80	85	90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly	95	100	105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser	110	115	120
Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys	125	130	135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly	140	145	150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu	155	160	165
Ser Lys Thr Ser Thr Ser Tyr Val	170		

<210> 333
 <211> 535
 <212> DNA
 <213> Homo sapiens

<400> 333
 agtgacaatc tcagagcagc ttctacacca cagccatttc cagcatgaag 50
 atcactgggg gtctccttct gctctgtaca gtggtctatt tctgtagcag 100
 ctcagaagct gctagtctgt ctccaaaaaa agtggactgc agcatttaca 150
 agaagtatcc agtgggtggcc atcccctgcc ccatcacata cctaccagtt 200
 tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250
 gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300
 aaattctcca tggacataga gagaaaggaa tgatattctc atcatcatct 350
 tcatcatccc aggctctgac tgagtttctt tcagttttac tgatgttctg 400
 ggtggggggac agagccagat tcagagtaat cttgactgaa tggagaaagt 450

ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcattttt 500
 tttttaacac gtcaataaaa aaataatctc ccaga 535

<210> 334
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 334
 Met Lys Ile Thr Gly Gly Leu Leu Leu Leu Cys Thr Val Val Tyr
 1 5 10 15
 Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
 20 25 30
 Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
 35 40 45
 Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
 50 55 60
 Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
 65 70 75
 Arg Val Gln Phe Leu His Asp Gly Ser Cys
 80 85

<210> 335
 <211> 742
 <212> DNA
 <213> Homo sapiens

<400> 335
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 ctgctcgcgc cccgccgcca tggtgcctc cccgcgcggg cctgctgtcc 100
 tggccctgac cgggctggcg ctgctcctgc tcctgtgctg gggcccaggt 150
 ggcataagtg gaaataaaact caagctgatg cttcaaaaac gagaagcacc 200
 tgttccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250
 tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300
 cccgaggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350
 agcgaaattt gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400
 gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450
 gcaattggtc cccggagccc ctacggcttt aggcattggag ccagcgtcaa 500
 ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaaatt 550
 agcgattctc ttcatgtatc tcctaattgcc ttacactact tggtttctga 600

tttgctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650
 gaagagttaa aacaacacat gtaaatgcct ttgatattt catgggaatg 700
 cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 336
 Met Ala Ala Ser Pro Ala Arg Pro Ala Val Leu Ala Leu Thr Gly
 1 5 10 15
 Leu Ala Leu Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser
 20 25 30
 Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val
 35 40 45
 Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu
 50 55 60
 Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg
 65 70 75
 Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met
 80 85 90
 Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu
 95 100 105
 Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln
 110 115 120
 Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr
 125 130 135
 Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr
 140 145

<210> 337
 <211> 1310
 <212> DNA
 <213> Homo sapiens

<400> 337
 cggctcgagc ccgcccggaa gtgcccgagg ggccgcgatg gagctggggg 50
 agccggggcg tcggtagcgc ggcgggcaag gcaggcgcca tgaccctgat 100
 tgaaggggtg ggtgatgagg tgaccgtcct tttctcggtg cttgcctgcc 150
 ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200
 gacccactgc ccagccgctc agggacccca acgcatccc agccagcgc 250

agccatggca gctaccgaca gcatgagagg ggaggcccca ggggcagaga 300
 cccccagcct gagacacaga ggtcaagctg cacagccaga gcccagcacg 350
 ggggttcacag caacaccgcc agccccggac tccccgcagg agcccctcgt 400
 gctacggctg aaattcctca atgattcaga gcagggtggcc agggcctggc 450
 cccacgacac cattggctcc ttgaaaagga cccagtttcc cggccgggaa 500
 cagcaggtgc gactcatcta ccaagggcag ctgctaggcg acgacacca 550
 gaccctgggc agccttcacc tccctcccaa ctgcgttctc cactgccacg 600
 tgtccacgag agtcgggtccc ccaaattccc cctgcccgcc ggggtccgag 650
 cccggccccct ccgggctgga aatcggcagc ctgctgctgc ccctgctgct 700
 cctgctgttg ctgctgctct ggtactgcca gatccagtac cggcccttct 750
 ttccccctgac cgccactctg ggccctggccg gcttcaccct gtcctcagt 800
 ctctggcct ttgccatgta ccgcccgtag tgccctccgcg ggcgcttggc 850
 agcgtcgccg gccctcccg accttgctcc ccgcgcgcgcg gcgggagctg 900
 ctgcctgccc agggccgcct ctccggcctg cctcttcccg ctgccctgga 950
 gcccagccct gcgcgcgaga ggactcccgg gactggcgga ggccccgccc 1000
 tgcgaccgcc ggggctcggg gccacctccc ggggctgctg aacctcagcc 1050
 cgactggga gtgggctcct cggggtcggg catctgctgt cgctgcctcg 1100
 gccccgggca gagccgggccc gccccggggg cccgtcttag tgttctgccg 1150
 gaggaccag ccgcctccaa tccctgacag ctccctgggg tgagttgggg 1200
 acgccaggtc ggtgggaggg tggtgaaggg gagcggggag gggcagagga 1250
 gttccccgga acccgtgcag attaaagtaa ctgtgaagtt ttaaaaaaaaa 1300
 aaaaaaaaaa 1310

<210> 338
 <211> 246
 <212> PRT
 <213> Homo sapiens

<400> 338
 Met Thr Leu Ile Glu Gly Val Gly Asp Glu Val Thr Val Leu Phe
 1 5 10 15
 Ser Val Leu Ala Cys Leu Leu Val Leu Ala Leu Ala Trp Val Ser
 20 25 30
 Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly
 35 40 45

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp	50	55	60
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg	65	70	75
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr	80	85	90
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu	95	100	105
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp	110	115	120
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly	125	130	135
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly	140	145	150
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys	155	160	165
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro	170	175	180
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile	185	190	195
Gly	Ser	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	200	205	210
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala	215	220	225
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala	230	235	240
Phe	Ala	Met	Tyr	Arg	Pro										245		

<210> 339

<211> 849

<212> DNA

<213> Homo sapiens

<400> 339

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tgccctctcc agattcccca ggctctcaga gaagatcagc agaaagtctg 100

caagacccta agaaccatca gccctcagct gcacctctc cctccaagg 150

atgacaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200

tcaggccagc ctcatcagtc gctgtgactt ggcccaggtg ctgcagctgg 250

aggacttggg tgggtttgag gggtactccc tgagtgactg gctgtgcctg 300
gcttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350
tggaagcttt gactatggcc tcttcagat caacagccac tactggtgca 400
acgattataa gagttactcg gaaaaccttt gccacgtaga ctgtcaagat 450
ctgctgaatc ccaaccttct tgcaggcatc cactgcgcaa aaaggattgt 500
gtccggagca cgggggatga acaactgggt agaattggagg ttgcactgtt 550
caggccggcc actctcctac tggctgacag gatgccgcct gagatgaaac 600
aggggtgcggg tgcaccgtgg agtcattcca agactcctgt cctcactcag 650
ggattcttca tttcttcttc ctactgcctc cacttcatgt tattttcttc 700
ccttccatt tacaactaaa actgaccaga gcccaggaa taaatggttt 750
tcttggttc ctccttactc ccatctggac ccagtcacct gggttcctgtc 800
tgttatttgt aaactgagga ccacaataaa gaaatcttta tatttatcg 849

<210> 340

<211> 148

<212> PRT

<213> Homo sapiens

<400> 340

Met	Thr	Lys	Ala	Leu	Leu	Ile	Tyr	Leu	Val	Ser	Ser	Phe	Leu	Ala	1	5	10	15
Leu	Asn	Gln	Ala	Ser	Leu	Ile	Ser	Arg	Cys	Asp	Leu	Ala	Gln	Val	20	25	30	
Leu	Gln	Leu	Glu	Asp	Leu	Asp	Gly	Phe	Glu	Gly	Tyr	Ser	Leu	Ser	35	40	45	
Asp	Trp	Leu	Cys	Leu	Ala	Phe	Val	Glu	Ser	Lys	Phe	Asn	Ile	Ser	50	55	60	
Lys	Ile	Asn	Glu	Asn	Ala	Asp	Gly	Ser	Phe	Asp	Tyr	Gly	Leu	Phe	65	70	75	
Gln	Ile	Asn	Ser	His	Tyr	Trp	Cys	Asn	Asp	Tyr	Lys	Ser	Tyr	Ser	80	85	90	
Glu	Asn	Leu	Cys	His	Val	Asp	Cys	Gln	Asp	Leu	Leu	Asn	Pro	Asn	95	100	105	
Leu	Leu	Ala	Gly	Ile	His	Cys	Ala	Lys	Arg	Ile	Val	Ser	Gly	Ala	110	115	120	
Arg	Gly	Met	Asn	Asn	Trp	Val	Glu	Trp	Arg	Leu	His	Cys	Ser	Gly	125	130	135	
Arg	Pro	Leu	Ser	Tyr	Trp	Leu	Thr	Gly	Cys	Arg	Leu	Arg						

<210> 341
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 341
 ccctccaagg atgacaaagg cgc 23

<210> 342
 <211> 29
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-29
 <223> Synthetic construct.

<400> 342
 ggtcagcagc tttcttgccc taaatcagg 29

<210> 343
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 343
 atctcaggcg gcatcctgtc agcc 24

<210> 344
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 344
 gtggatgcct gcaagaaggt tggg 24

<210> 345
 <211> 45
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 345
agctttcttg ccctaaatca ggccagcctc atcagtcgct gtgac 45

<210> 346
<211> 2575
<212> DNA
<213> Homo sapiens

<400> 346
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<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

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Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly	
				65					70					75	
Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu	
				80					85					90	
Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg	
				95					100					105	
Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile	
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Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp	
				125					130					135	
Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr	
				140					145					150	
Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala	
				155					160					165	
Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu	
				170					175					180	
Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val	
				185					190					195	
Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr	
				200					205					210	
Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu	
				215					220					225	
Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser	
				230					235					240	
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu	
				245					250					255	

Arg Ser Asn Lys	Arg Leu Gly Ala Ile	Arg Ala Arg Met Leu Gly	260	265	270
Ala Thr Arg Ala	Thr Gly Asp Val Leu	Val Phe Met Asp Ala His	275	280	285
Cys Glu Cys His	Pro Gly Trp Leu Glu	Pro Leu Leu Ser Arg Ile	290	295	300
Ala Gly Asp Arg	Ser Arg Val Val Ser	Pro Val Ile Asp Val Ile	305	310	315
Asp Trp Lys Thr	Phe Gln Tyr Tyr Pro	Ser Lys Asp Leu Gln Arg	320	325	330
Gly Val Leu Asp	Trp Lys Leu Asp Phe	His Trp Glu Pro Leu Pro	335	340	345
Glu His Val Arg	Lys Ala Leu Gln Ser	Pro Ile Ser Pro Ile Arg	350	355	360
Ser Pro Val Val	Pro Gly Glu Val Val	Ala Met Asp Arg His Tyr	365	370	375
Phe Gln Asn Thr	Gly Ala Tyr Asp Ser	Leu Met Ser Leu Arg Gly	380	385	390
Gly Glu Asn Leu	Glu Leu Ser Phe Lys	Ala Trp Leu Cys Gly Gly	395	400	405
Ser Val Glu Ile	Leu Pro Cys Ser Arg	Val Gly His Ile Tyr Gln	410	415	420
Asn Gln Asp Ser	His Ser Pro Leu Asp	Gln Glu Ala Thr Leu Arg	425	430	435
Asn Arg Val Arg	Ile Ala Glu Thr Trp	Leu Gly Ser Phe Lys Glu	440	445	450
Thr Phe Tyr Lys	His Ser Pro Glu Ala	Phe Ser Leu Ser Lys Ala	455	460	465
Glu Lys Pro Asp	Cys Met Glu Arg Leu	Gln Leu Gln Arg Arg Leu	470	475	480
Gly Cys Arg Thr	Phe His Trp Phe Leu	Ala Asn Val Tyr Pro Glu	485	490	495
Leu Tyr Pro Ser	Glu Pro Arg Pro Ser	Phe Ser Gly Lys Leu His	500	505	510
Asn Thr Gly Leu	Gly Leu Cys Ala Asp	Cys Gln Ala Glu Gly Asp	515	520	525
Ile Leu Gly Cys	Pro Met Val Leu Ala	Pro Cys Ser Asp Ser Arg	530	535	540
Gln Gln Gln Tyr	Leu Gln His Thr Ser	Arg Lys Glu Ile His Phe			

	545		550		555
Gly Ser Pro Gln His Leu Cys Phe Ala Val Arg Gln Glu Gln Val	560		565		570
Ile Leu Gln Asn Cys Thr Glu Glu Gly Leu Ala Ile His Gln Gln	575		580		585
His Trp Asp Phe Gln Glu Asn Gly Met Ile Val His Ile Leu Ser	590		595		600
Gly Lys Cys Met Glu Ala Val Val Gln Glu Asn Asn Lys Asp Leu	605		610		615
Tyr Leu Arg Pro Cys Asp Gly Lys Ala Arg Gln Gln Trp Arg Phe	620		625		630
Asp Gln Ile Asn Ala Val Asp Glu Arg	635				

<210> 348
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 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

 <400> 348
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 <210> 349
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 349
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 <210> 350
 <211> 45
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

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<210> 351
<211> 2524
<212> DNA
<213> Homo sapiens

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<210> 352

<212> PRT

<213> Homo sapiens

<400> 352

Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly
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5

10

15

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<210> 354

<211> 121

<212> PRT

<213> Homo sapiens

<400> 354

Met	Ala	Ser	Cys	Leu	Ala	Leu	Arg	Met	Ala	Leu	Leu	Leu	Val	Ser
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				20					25					30
Pro	Val	Pro	Thr	Leu	Trp	Asn	Glu	Pro	Ala	Glu	Leu	Pro	Ser	Gly
				35					40					45
Glu	Gly	Pro	Val	Glu	Ser	Thr	Ser	Pro	Gly	Arg	Glu	Pro	Val	Asp
				50					55					60
Thr	Gly	Pro	Pro	Ala	Pro	Thr	Val	Ala	Pro	Gly	Pro	Glu	Asp	Ser
				65					70					75
Thr	Ala	Gln	Glu	Arg	Leu	Asp	Gln	Gly	Gly	Gly	Ser	Leu	Gly	Pro
				80					85					90
Gly	Ala	Ile	Ala	Ala	Ile	Val	Ile	Ala	Ala	Leu	Leu	Ala	Thr	Cys
				95					100					105
Val	Val	Leu	Ala	Leu	Val	Val	Val	Ala	Leu	Arg	Lys	Phe	Ser	Ala
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Ser

<210> 355

<211> 2134

<212> DNA

<213> Homo sapiens

<400> 355

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<210> 356

<211> 157

<212> PRT

<213> Homo sapiens

<400> 356

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His Gly Cys Leu His Cys His Ser Asn Phe Ser Lys Lys Phe Ser
 20 25 30

Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val Gly Asp
 35 40 45

Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp Thr
 50 55 60

Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu
 65 70 75

Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln
 80 85 90

Leu Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu
 95 100 105

Leu Arg Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala
 110 115 120

Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gly Gln
 125 130 135

Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro

140

145

150

Ser Pro Arg Gly Asp Leu Pro
155

<210> 357

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 357

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tctcttcttc ottcttttaa atttcatatc ctactccct atccaatttc 1100
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tcaaggcttt aagagactca ctgtgatgcc tctatgaaag agaggcattc 1200

ctagagaaag attgttccaa tttgtcattt aatatcaagt ttgtatactg 1250
cacatgactt acacacaaca tagttcctgc tcttttaagg ttacctaagg 1300
gttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350
tcaaaaacca aaggatgggt ttaaacacct ttgtgaaatt gtctttttgc 1400
cagaagttaa aggctgtctc caagtccttg aactcagcag aaatagacca 1450
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caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met	Glu	Ala	Ala	Pro	Ser	Arg	Phe	Met	Phe	Leu	Leu	Phe	Leu	Leu
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Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser
				20					25					30
Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp
				35					40					45
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val
				50					55					60
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu
				65					70					75
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser
				80					85					90
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr
				95					100					105
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu
				110					115					120
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe
				125					130					135
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val
				140					145					150
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu
				155					160					165
Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His
				170					175					180
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe
				185					190					195

Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser
				200					205					210
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr
				215					220					225
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val
				230					235					240
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly
				245					250					255
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys
				260					265					270

Val Glu Leu

<210> 359
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 359
 ccagcagtgc ccatactcca tagc 24

<210> 360
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 360
 tgacgagtgg gatacactgc 20

<210> 361
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 361
 gctctacgga aacttctgct gtgg 24

<210> 362

<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 362
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363
<211> 1777
<212> DNA
<213> Homo sapiens

<400> 363
ggagagccgc ggctgggacc ggagtgggga ggcgcggcgtg gaggtgccac 50
ccggcgcggg tggcggagag atcagaagcc tcttcccca gccgagccaa 100
cctcagcggg gacccgggct cagggacgcg gcggcgggcg cggcgactgc 150
agtggctgga cgatggcagc gtccgccgga gccggggcg tgattgcagc 200
cccagacagc cggcgctggc tgtggtcggt gctggcgggc gcgcttgggc 250
tcttgacagc tggagtatca gccttggaag tatatacgcc aaaagaaatc 300
ttcgtggcaa atggtacaca aggaagctg acctgcaagt tcaagtctac 350
tagtacgact ggcggggttg cctcagtctc ctggagcttc cagccagagg 400
gggccgacac tactgtgtcg tttttccact actcccaagg gcaagtgtac 450
cttggggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500
tgacaagaaa gatgcatcaa tcaacataga aaatatgcag ttatatacaca 550
atggcaccta tatctgtgat gtcaaaaacc ctctgacat cgttgtccag 600
cctggacaca ttaggctcta tgtcgtagaa aaagagaatt tgctgtgtt 650
tccagtttgg gtagtggtgg gcatagttac tgctgtggtc ctaggtctca 700
ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750
aaacgggatt aactggctg cagtacatca gagagtttgt caccagttaa 800
gcaggctcct cggaagtccc cctccgacac tgagggtctt gtaaagagtc 850
tgccttctgg atctcaccag ggcccagtc tatatgcaca gttagaccac 900
tccggcggac atcacagtga caagattaac aagtcagagt ctgtggtgta 950
tgcggatata cgaaagaatt aagagaatac ctagaacata tcctcagcaa 1000

[illegible]

<211> 269

<213> Homo sapiens

Met Ala Ala Ser Ala Gly Ala Gly Ala Val Ile Ala Ala Pro Asp
1 5 10 15

Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp
95 100 105

Year	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

<211> 1321

<212> DNA

<213> Homo sapiens

<400> 365

349

cgaattgcta gcatcagcaa aagtctcacc atggttgctc ttgccaaatt 550
 gtgggaagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600
 ccgaattccc agaaaaagaa tatgaagggtg aaaagggttc tgtcacaaca 650
 agattactga tttcccatTT aagtgggaatt cgtcattatg aaaaggacat 700
 aaaaaagggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750
 agaatgtttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800
 gattttacta aatttaaaac agagcaggag aatgaagcca aatgccggaa 850
 ttcaaaacct ggcaagaaaa agaattgattt tgaacaaggc gaattatatt 900
 tgagagaaaa gtttgaaaat tcaattgaat ccctaagatt atttaaaaaat 950
 gatcctttgt tcttcaaacc tggtagtcag tttttgtatt caacttttgg 1000
 ctatacccta ctggcagcca tagtagagag agcttcagga tgtaaattatt 1050
 tggactatat gcagaaaata ttccatgact tggatatgct gacgactgtg 1100
 caggaagaaa acgagccagt gatttacaat agagcaagggt aaatgaatac 1150
 cttctgctgt gtctagctat atcgcatctt aacactattt tattaattaa 1200
 aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacatttttg 1250
 gagcttttct acatgtctgt tttctcatct gtaaagtgaa ggaagtaaaa 1300
 catgtttata aagtaaaaaa a 1321

<210> 366
 <211> 373
 <212> PRT
 <213> Homo sapiens

<400> 366
 Met Tyr Arg Leu Leu Ser Ala Val Thr Ala Arg Ala Ala Ala Pro
 1 5 10 15
 Gly Gly Leu Ala Ser Ser Cys Gly Arg Arg Gly Val His Gln Arg
 20 25 30
 Ala Gly Leu Pro Pro Leu Gly His Gly Trp Val Gly Gly Leu Gly
 35 40 45
 Leu Gly Leu Gly Leu Ala Leu Gly Val Lys Leu Ala Gly Gly Leu
 50 55 60
 Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu
 65 70 75
 Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro
 80 85 90

<211> 30
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-30
 <223> Synthetic construct.

<400> 367
 tggaaaagaa gtctgggtcag aaggtttagg 30

<210> 368
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 368
 catttggctt cattctcctg ctctg 25

<210> 369
 <211> 28
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-28
 <223> Synthetic construct.

<400> 369
 aaaacctcag aacaactcat ttgacacc 28

<210> 370
 <211> 41
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-41
 <223> Synthetic construct.

<400> 370
 gtctcaccat ggttgctctt gccaaattgt gggaagcagg g 41

<210> 371
 <211> 1150
 <212> DNA
 <213> Homo sapiens

<400> 371
 gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggctggt gggaagaagc cgagatggcg gcagccagcg 100
 ctggggcaac cgggctgctc ctgctcttgc tgatggcggt agcagcgccc 150
 agtcgagccc ggggcagcgg ctgccgggcc gggactggtg cgcgaggggc 200
 tggggcggaa ggtcgagagg gcgaggcctg tggcacggtg gggctgctgc 250
 tggagcactc atttgagatc gatgacagt ccaacttccg gaagcggggc 300
 tcaactgctct ggaaccagca ggatggtacc ttgtccctgt cacagcggca 350
 gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400
 gcctgtaccg ggtccggatc ccaaggcgac ccggggccct ggatggcctg 450
 gaagctggtg gctatgtctc ctcttttgc cctgctgct ccctggtgga 500
 gtcgcacctg tcggaccagc tgaccctgca cgtggatgtg gccggcaacg 550
 tgggtggcgt gtcggtggtg acgcaccccg ggggctgccg gggccatgag 600
 gtggaggacg tggacctgga gctgttcaac acctcgggtg agctgcagcc 650
 gcccaccaca gcccaggcc ctgagacggc ggccttcatt gagcgcctgg 700
 agatggaaca ggcccagaag gccaaagaacc cccaggagca gaagtccttc 750
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 gtcaggagcg ccagacaccg ggggccaggg tgggggtggg ggtgggggtg 850
 gtggtggggg tagtggcctt tgctgtgtgc caccctccct gtaagtctat 900
 ttaaaaacat cgacgataca ttgaaatgtg tgaacgtttt gaaaagctac 950
 agcttccagc agccaaaagc aactgttggt ttggcaagac ggtcctgatg 1000
 tacaagcttg attgaaattc actgctcact tgatacgta ttcagaaacc 1050
 caaggaatgg ctgtccocat cctcatgtgg ctgtgtggag ctcagctgtg 1100
 ttgtgtggca gtttattaaa ctgtcccca gatcgacacg caaaaaaaaa 1150

<210> 372
 <211> 269
 <212> PRT
 <213> Homo sapiens

<400> 372
 Met Ala Ala Ala Ser Ala Gly Ala Thr Arg Leu Leu Leu Leu Leu
 1 5 10 15
 Leu Met Ala Val Ala Ala Pro Ser Arg Ala Arg Gly Ser Gly Cys
 20 25 30
 Arg Ala Gly Thr Gly Ala Arg Gly Ala Gly Ala Glu Gly Arg Glu
 35 40 45

Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	
				50					55					60	
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	
				65					70					75	
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	
				80					85					90	
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	
				95					100					105	
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	
				110					115					120	
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	
				125					130					135	
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	
				140					145					150	
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	
				155					160					165	
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	
				170					175					180	
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	
				185					190					195	
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	
				200					205					210	
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	
				215					220					225	
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	
				230					235					240	
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
				245					250					255	
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		
				260					265						

<210> 373
 <211> 1706
 <212> DNA
 <213> Homo sapiens

<400> 373
 ggagcgctgc tggaaaccca gccggagccg gagccacagc ggggaggggtg 50
 gcctggcggc ctggagccgg acgtgtccgg ggcgtccccg cagaccgggg 100
 cagcaggtcg tccggggggc caccatgctg gtgactgcct accttgcttt 150
 tgtaggcctc ctggcctcct gcctgggggt ggaactgtca agatgccggg 200

ctaaaccccc tggaagggcc tgcagcaatc cctccttcct tcggtttcaa 250
ctggacttct atcaggtcta cttcctggcc ctggcagctg attggcttca 300
ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggtc 350
aaattgccat cctctatgtc tgtggccttg cctctacagt cctctttggc 400
ctagtggcct cctcccttgt ggattggctg ggtcgcaaga attcttgtgt 450
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actactttgt gctgctagtg gggcgagcac ttggtgggct gtccacagcc 550
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gcatgacttc cctgctgagt ggatcccagc tacctttgct cgagctgcct 650
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cacacggggc ccctctgggc attatcttct ccagcttcat ggcagccagc 1000
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tcttcatgtt gactttctct accagcccag gccaggagag tccggtggag 1150
tccttcatag cctttctact tattgagttg gcttgtggat tatactttcc 1200
cagcatgagc ttctacgga gaaaggatgat ccctgagaca gagcaggctg 1250
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gactgacttt gtgactgtcc tgtggtttct cctgccattg ctttgtgttt 1600
gggaggacat gatgggggtg atggactgga aagaagggtc caaaagttcc 1650

ctctgtgttta ctccatttta gaaaataaac actttttaaat gatcaaaaaa 1700

aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met	Leu	Val	Thr	Ala	Tyr	Leu	Ala	Phe	Val	Gly	Leu	Leu	Ala	Ser
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Cys	Leu	Gly	Leu	Glu	Leu	Ser	Arg	Cys	Arg	Ala	Lys	Pro	Pro	Gly
				20					25					30

Arg	Ala	Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe
				35					40					45

Tyr	Gln	Val	Tyr	Phe	Leu	Ala	Leu	Ala	Ala	Asp	Trp	Leu	Gln	Ala
				50					55					60

Pro	Tyr	Leu	Tyr	Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly
				65					70					75

Gln	Ile	Ala	Ile	Leu	Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu
				80					85					90

Phe	Gly	Leu	Val	Ala	Ser	Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys
				95					100					105

Asn	Ser	Cys	Val	Leu	Phe	Ser	Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu
				110					115					120

Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	Val	Leu	Leu	Val	Gly	Arg	Ala
				125					130					135

Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Ser	Ala	Phe	Glu	Ala
				140					145					150

Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	Asp	Phe	Pro	Ala	Glu
				155					160					165

Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	Trp	Asn	His	Val
				170					175					180

Leu	Ala	Val	Val	Ala	Gly	Val	Ala	Ala	Glu	Ala	Val	Ala	Ser	Trp
				185					190					195

Ile	Gly	Leu	Gly	Pro	Val	Ala	Pro	Phe	Val	Ala	Ala	Ile	Pro	Leu
				200					205					210

Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn
				215					220					225

Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu
				230					235					240

Arg Cys Leu Leu Ser Asp Arg Arg Val Leu Leu Leu Gly Thr Ile
245 250 255

Gln Ala Leu Phe Glu Ser Val Ile Phe Ile Phe Val Phe Leu Trp
260 265 270

Thr Pro Val Leu Asp Pro His Gly Ala Pro Leu Gly Ile Ile Phe
275 280 285

Ser Ser Phe Met Ala Ala Ser Leu Leu Gly Ser Ser Leu Tyr Arg
290 295 300

Ile Ala Thr Ser Lys Arg Tyr His Leu Gln Pro Met His Leu Leu
305 310 315

Ser Leu Ala Val Leu Ile Val Val Phe Ser Leu Phe Met Leu Thr
320 325 330

Phe Ser Thr Ser Pro Gly Gln Glu Ser Pro Val Glu Ser Phe Ile
335 340 345

Ala Phe Leu Leu Ile Glu Leu Ala Cys Gly Leu Tyr Phe Pro Ser
350 355 360

Met Ser Phe Leu Arg Arg Lys Val Ile Pro Glu Thr Glu Gln Ala
365 370 375

Gly Val Leu Asn Trp Phe Arg Val Pro Leu His Ser Leu Ala Cys
380 385 390

Leu Gly Leu Leu Val Leu His Asp Ser Asp Arg Lys Thr Gly Thr
395 400 405

Arg Asn Met Phe Ser Ile Cys Ser Ala Val Met Val Met Ala Leu
410 415 420

Leu Ala Val Val Gly Leu Phe Thr Val Val Arg His Asp Ala Glu
425 430 435

Leu Arg Val Pro Ser Pro Thr Glu Glu Pro Tyr Ala Pro Glu Leu
440 445 450

<210> 375
<211> 1098
<212> DNA
<213> Artificial

<400> 375
gcgacgcgcg gcggggcggc gagaggaaac gcggcgcccg gccgggcccg 50
gccctggaga tgggtccccg cgccgcgggc tgggtgtgtc tcgtgctctg 100
gctccccgcg tgcgtgcgcg cccacggctt ccgtatccat gattatttgt 150
actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200
cctgccaaag actttggtgg tatctttcac acaaggtatg agcagattca 250

ccttggtcccc gctgaacctc cagaggcctg cggggaactc agcaacggtt 300
tcttcatcca ggaccagatt gctctggtgg agaggggggg ctgctccttc 350
ctctccaaga ctcggttggt ccaggagcac ggcgggcggg cggtgatcat 400
ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450
acagtaccca gcgcacagct gacatccccg ccctcttcct gctcggccga 500
gacggctaca tgatcogcog ctctctggaa cagcatgggc tgccatgggc 550
catcatttcc atcccagtc aatgcaccag catccccacc tttgagctgc 600
tgcaaccgcc ctggaccttc tggtagaaga gtttgtccca cattccagcc 650
ataagtgaact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700
aatattggaga tagcatctgg ggacaagtgg agccaggtag aggaaaaggg 750
tttgggcgtt gctaggctga aagggaagcc acaccactgg ccttcccttc 800
cccagggccc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850
ccccagggct tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900
gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950
taccaggggt ctctgcacag tgaccttcac agcagttggt ggagtgggtt 1000
aaagagctgg tgtttgggga ctcaataaac cctcactgac tttttagcaa 1050
taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
1				5				10						15
Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
				20				25						30
Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
				35				40						45
Ala	Thr	Pro	Ala	Lys	Asp	Phe	Gly	Gly	Ile	Phe	His	Thr	Arg	Tyr
				50				55						60
Glu	Gln	Ile	His	Leu	Val	Pro	Ala	Glu	Pro	Pro	Glu	Ala	Cys	Gly
				65				70						75
Glu	Leu	Ser	Asn	Gly	Phe	Phe	Ile	Gln	Asp	Gln	Ile	Ala	Leu	Val
				80				85						90

Glu	Arg	Gly	Gly	Cys	Ser	Phe	Leu	Ser	Lys	Thr	Arg	Val	Val	Gln
				95					100					105
Glu	His	Gly	Gly	Arg	Ala	Val	Ile	Ile	Ser	Asp	Asn	Ala	Val	Asp
				110					115					120
Asn	Asp	Ser	Phe	Tyr	Val	Glu	Met	Ile	Gln	Asp	Ser	Thr	Gln	Arg
				125					130					135
Thr	Ala	Asp	Ile	Pro	Ala	Leu	Phe	Leu	Leu	Gly	Arg	Asp	Gly	Tyr
				140					145					150
Met	Ile	Arg	Arg	Ser	Leu	Glu	Gln	His	Gly	Leu	Pro	Trp	Ala	Ile
				155					160					165
Ile	Ser	Ile	Pro	Val	Asn	Val	Thr	Ser	Ile	Pro	Thr	Phe	Glu	Leu
				170					175					180
Leu	Gln	Pro	Pro	Trp	Thr	Phe	Trp							
				185										

<210> 377
 <211> 496
 <212> DNA
 <213> Artificial

<220>
 <221> unsure
 <222> 396
 <223> unknown base

<400> 377
 tctgcctcca ctgctctgtg ctgggatcat ggaacttgca ctgctgtgtg 50
 ggctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100
 ctgaacaaga tgggtcaagca agtgactggg aaaatgccca tcctctccta 150
 ctggccctac ggctgtcact gcggactagg tggcagaggc caaccctaaag 200
 atgccacgga ctggtgctgc cagaccocatg actgctgcta tgaccacctg 250
 aagaccacagg ggtgcggcat ctacaaggac aacaacaaaa gcagcataca 300
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val
1				5					10					15
Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys
			20						25					30
Gln	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly
			35						40					45
Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr
			50						55					60
Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys
			65						70					75
Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile
			80						85					90
His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe
			95						100					105
Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu				
			110						115					

<210> 379
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 379
 ctgcctccac tgctctgtgc tggg 24

 <210> 380
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 380
 cagagcagtg gatgttcccc tggg 24

 <210> 381
 <211> 45
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-45

<223> Synthetic construct.

<400> 381
ctgaacaaga tgggtcaagca agtgactggg aaaatgccca tcctc 45

<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382
ctcgcttctt ccttctggat gggggcccag gggggcccagg agagtataaa 50
ggcgatgtgg aggggtgcccg gcacaaccag acgcccagtc acaggcgaga 100
gccctgggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150
ctcctggggg gccccacctg ggcagggaag atgtatggcc ctggaggagg 200
caagtatttc agcaccactg aagactacga ccatgaaatc acagggctgc 250
gggtgtctgt aggtcttctc ctggtgaaaa gtgtccagggt gaaacttgga 300
gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350
caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400
ctttcctccg gggatatggc atgtacacca gcaaggaccg ctatttctat 450
tttggaagc ttgatggcca gatctctctt gcctaccca gccaaaggagg 500
gcagggtgctg gtgggcatct atggccagta tcaactcctt ggcatcaaga 550
gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600
ccagttaatc tcacatactc agcaaactca cccgtgggtc gctaggggtg 650
ggatatggggc catccgagct gaggccatct gtgtgggtgt ggctgatggt 700
actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750
gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383
Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu
1 5 10 15
Leu Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly
20 25 30
Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr
35 40 45

Gly	Leu	Arg	Val	Ser	Val	Gly	Leu	Leu	Leu	Val	Lys	Ser	Val	Gln
				50					55					60
Val	Lys	Leu	Gly	Asp	Ser	Trp	Asp	Val	Lys	Leu	Gly	Ala	Leu	Gly
				65					70					75
Gly	Asn	Thr	Gln	Glu	Val	Thr	Leu	Gln	Pro	Gly	Glu	Tyr	Ile	Thr
				80					85					90
Lys	Val	Phe	Val	Ala	Phe	Gln	Ala	Phe	Leu	Arg	Gly	Met	Val	Met
				95					100					105
Tyr	Thr	Ser	Lys	Asp	Arg	Tyr	Phe	Tyr	Phe	Gly	Lys	Leu	Asp	Gly
				110					115					120
Gln	Ile	Ser	Ser	Ala	Tyr	Pro	Ser	Gln	Glu	Gly	Gln	Val	Leu	Val
				125					130					135
Gly	Ile	Tyr	Gly	Gln	Tyr	Gln	Leu	Leu	Gly	Ile	Lys	Ser	Ile	Gly
				140					145					150
Phe	Glu	Trp	Asn	Tyr	Pro	Leu	Glu	Glu	Pro	Thr	Thr	Glu	Pro	Pro
				155					160					165
Val	Asn	Leu	Thr	Tyr	Ser	Ala	Asn	Ser	Pro	Val	Gly	Arg		
				170					175					

<210> 384
 <211> 2379
 <212> DNA
 <213> Homo sapiens

<400> 384
 gctgagcgtg tgcgcggtac ggggctctcc tgccttctgg gctccaacgc 50
 agctctgtgg ctgaactggg tgctcatcac gggaactgct gggctatgga 100
 atacagatgt ggcagctcag gtagcccca attgcctgga agaatacatc 150
 atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200
 cccctcccca ccccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250
 atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300
 tgttgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350
 atgttccaaa atcgggtccat ctoccaaagg gtccaatttt tcttcctggg 400
 tgtcagcgag ccctgactca ctacagtga gctgacagg gctgtcatgc 450
 aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500
 acaaaggatg ggtttcaatg taattaggct actgagcgga tcagctgtag 550
 cactggttat agccccact gtcttactga caatgctttc ttctgccgaa 600
 cgaggatgcc ctaagggctg taggtgtgaa ggcaaaatgg tatattgtga 650

atctcagaaa ttacaggaga taccctcaag tatactctgct ggttgcttag 700
 gtttgtccct tcgctataac agccttcaaa aacttaagta taatcaattt 750
 aaagggtcct accagctcac ctggctatac cttgaccata accatatcag 800
 caatatggac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850
 ttcttagttc caatagaatc tcctattttc ttaacaatac cttcagacct 900
 gtgacaaaatt tacggaaactt ggatctgtcc tataatcagc tgcattctct 950
 gggatctgaa cagtttcggg gcttgcgga gctgctgagt ttacatttac 1000
 ggtctaactc cctgagaacc atccctgtgc gaatattcca agactgccgc 1050
 aacctggaac ttttggaact gggatataac cggatccgaa gtttagccag 1100
 gaatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150
 atcaattttc caagctcaac ctggcccttt ttccaagggt ggtcagcctt 1200
 cagaaccttt acttgcaagt gaataaaatc agtgtcatag gacagaccat 1250
 gtcctggacc tggagctcct taaaaaggct tgatttatca ggcaatgaga 1300
 tcgaagcttt cagtggacct agtgttttcc agtgtgtccc gaactctgag 1350
 cgcctcaacc tggattccaa caagctcaca tttattggc aagagatttt 1400
 ggattcttgg atatccctca atgacatcag tcttgctggg aatatatggg 1450
 aatgcagcag aaatatttgc tcccttgtaa actggctgaa aagttttaaa 1500
 ggtctaaggg agaatacaat tatctgtgcc agtcccaaag agctgcaagg 1550
 agtaaagtgt atcgatgcag tgaagaacta cagcatctgt ggcaaaagta 1600
 ctacagagag gtttgatctg gccagggtc tcccaaagcc gacgtttaag 1650
 cccaagctcc ccaggccgaa gcatgagagc aaacccctt tgccccgac 1700
 ggtgggagcc acagagcccg gccagagac cgatgctgac gccgagcaca 1750
 tctctttcca taaaatcacc gggggcagcg tggcgctttt cctgtccgtg 1800
 ctctcatcc tgctggttat ctacgtgtca tggaagcgg accctgcgag 1850
 catgaagcag ctgcagcagc gctccctcat gcgaaggcac agggaaaaaga 1900
 aaagacagtc cctaaagcaa atgactccca gcaccagga attttatgta 1950
 gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatgggac 2000
 gggaccctgc acctataaca aatcgggtc caggagagt gaggtatgaa 2050
 ccattgtgat aaaaagagct cttaaaagct gggaaataag tggtgcttta 2100

ttgaactctg gtgactatca agggaacgag atgccccccc tccccttccc 2150
 tctccctctc actttggtgg caagatcctt ccttgtccgt tttagtgcac 2200
 tcataatact ggtcattttc ctctcatata taatcaaccc attgaaattt 2250
 aaataccaca atcaatgtga agcttgaact ccggtttaat ataataccta 2300
 ttgtataaga ccctttactg attccattaa tgtcgcattt gttttaagat 2350
 aaaacttctt tcataggtaa aaaaaaaaaa 2379

<210> 385

<211> 513

<212> PRT

<213> Homo sapiens

<400> 385

Met	Gly	Phe	Asn	Val	Ile	Arg	Leu	Leu	Ser	Gly	Ser	Ala	Val	Ala
1				5					10					15
Leu	Val	Ile	Ala	Pro	Thr	Val	Leu	Leu	Thr	Met	Leu	Ser	Ser	Ala
				20					25					30
Glu	Arg	Gly	Cys	Pro	Lys	Gly	Cys	Arg	Cys	Glu	Gly	Lys	Met	Val
				35					40					45
Tyr	Cys	Glu	Ser	Gln	Lys	Leu	Gln	Glu	Ile	Pro	Ser	Ser	Ile	Ser
				50					55					60
Ala	Gly	Cys	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn	Ser	Leu	Gln	Lys
				65					70					75
Leu	Lys	Tyr	Asn	Gln	Phe	Lys	Gly	Leu	Asn	Gln	Leu	Thr	Trp	Leu
				80					85					90
Tyr	Leu	Asp	His	Asn	His	Ile	Ser	Asn	Ile	Asp	Glu	Asn	Ala	Phe
				95					100					105
Asn	Gly	Ile	Arg	Arg	Leu	Lys	Glu	Leu	Ile	Leu	Ser	Ser	Asn	Arg
				110					115					120
Ile	Ser	Tyr	Phe	Leu	Asn	Asn	Thr	Phe	Arg	Pro	Val	Thr	Asn	Leu
				125					130					135
Arg	Asn	Leu	Asp	Leu	Ser	Tyr	Asn	Gln	Leu	His	Ser	Leu	Gly	Ser
				140					145					150
Glu	Gln	Phe	Arg	Gly	Leu	Arg	Lys	Leu	Leu	Ser	Leu	His	Leu	Arg
				155					160					165
Ser	Asn	Ser	Leu	Arg	Thr	Ile	Pro	Val	Arg	Ile	Phe	Gln	Asp	Cys
				170					175					180
Arg	Asn	Leu	Glu	Leu	Leu	Asp	Leu	Gly	Tyr	Asn	Arg	Ile	Arg	Ser
				185					190					195
Leu	Ala	Arg	Asn	Val	Phe	Ala	Gly	Met	Ile	Arg	Leu	Lys	Glu	Leu

	200		205		210
His Leu Glu His	Asn Gln Phe Ser Lys	Leu Asn Leu Ala Leu Phe			
	215	220			225
Pro Arg Leu Val	Ser Leu Gln Asn Leu Tyr	Leu Gln Trp Asn Lys			
	230	235			240
Ile Ser Val Ile	Gly Gln Thr Met Ser Trp	Thr Trp Ser Ser Leu			
	245	250			255
Gln Arg Leu Asp	Leu Ser Gly Asn Glu Ile	Glu Ala Phe Ser Gly			
	260	265			270
Pro Ser Val Phe	Gln Cys Val Pro Asn Leu	Gln Arg Leu Asn Leu			
	275	280			285
Asp Ser Asn Lys	Leu Thr Phe Ile Gly Gln	Glu Ile Leu Asp Ser			
	290	295			300
Trp Ile Ser Leu	Asn Asp Ile Ser Leu Ala	Gly Asn Ile Trp Glu			
	305	310			315
Cys Ser Arg Asn	Ile Cys Ser Leu Val Asn	Trp Leu Lys Ser Phe			
	320	325			330
Lys Gly Leu Arg	Glu Asn Thr Ile Ile Cys	Ala Ser Pro Lys Glu			
	335	340			345
Leu Gln Gly Val	Asn Val Ile Asp Ala Val	Lys Asn Tyr Ser Ile			
	350	355			360
Cys Gly Lys Ser	Thr Thr Glu Arg Phe Asp	Leu Ala Arg Ala Leu			
	365	370			375
Pro Lys Pro Thr	Phe Lys Pro Lys Leu Pro	Arg Pro Lys His Glu			
	380	385			390
Ser Lys Pro Pro	Leu Pro Pro Thr Val Gly	Ala Thr Glu Pro Gly			
	395	400			405
Pro Glu Thr Asp	Ala Asp Ala Glu His Ile	Ser Phe His Lys Ile			
	410	415			420
Ile Ala Gly Ser	Val Ala Leu Phe Leu Ser	Val Leu Val Ile Leu			
	425	430			435
Leu Val Ile Tyr	Val Ser Trp Lys Arg Tyr	Pro Ala Ser Met Lys			
	440	445			450
Gln Leu Gln Gln	Arg Ser Leu Met Arg Arg	His Arg Lys Lys Lys			
	455	460			465
Arg Gln Ser Leu	Lys Gln Met Thr Pro Ser	Thr Gln Glu Phe Tyr			
	470	475			480
Val Asp Tyr Lys	Pro Thr Asn Thr Glu Thr	Ser Glu Met Leu Leu			
	485	490			495

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
 500 505 510

Cys Glu Val

<210> 386
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 386
 ctgggatctg aacagtttcg gggc 24

<210> 387
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 387
 ggtccccagg acatggtctg tccc 24

<210> 388
 <211> 48
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-48
 <223> Synthetic construct.

<400> 388
 gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389
 <211> 1449
 <212> DNA
 <213> Homo sapiens

<400> 389
 agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50
 ttgactgtcc tttaaatatg tcaagatcca gacttttcag tgtcacctca 100
 gcgatctcaa cgatagggat cttgtgtttg ccgctattcc agttggtgct 150
 ctcggaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

aacaccctaa tggctggtat atctggatcc tcctgctgct ggttttggtg 250
 gcagctcttc tctgtggagc tgtggtcctc tgcctccagt gctggctgag 300
 gagaccccgga attgattctc acaggcgcac catggcagtt tttgctggtg 350
 gagacttgga ctctatttat gggacagaag cagctgtgag tccaactggt 400
 ggaattcacc ttcaaactca aaccctgac ctatatcctg ttctgctcc 450
 atgttttggc cctttaggct cccacctcc atatgaagaa attgtaaaaa 500
 caacctgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550
 taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600
 tccagagatc tattcatata gtctgaggaa ggacaattcg acaaaagaat 650
 ggatgttgga aaaaattttg gtcattggaga tgtttaaata gtaaagtagc 700
 aggcctttga tgtgtcactg ctgtatcata cttttatgct acacaaccaa 750
 attaagtctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800
 gtagtttcca tcacatttag gactccactg cagtatacag cacaccattt 850
 tctgctttaa actctttcct agcatggggt ccataaaaat tattataatt 900
 taacaatagc ccaagccgag aatccaacat gtccagaacc agaaccagaa 950
 agatagtatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000
 tggagttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050
 gtctcagcaa aaacaagagg ttttatgccc caacctgaag aggaagaaat 1100
 tgtagataga aggtgaagga gattgctgaa gatatagagc acatataatg 1150
 ccaacacggg gagaaaagaa aatttccct tttacagtaa tgaatgtggc 1200
 ctccatagtc catagtgttt ctctggagcc tcaggggcttg gcatttattg 1250
 cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300
 gcagaagtag caatgagaca tcttcaagtg gcattttggc agtggccatc 1350
 agcaggggga cagacaaaaa catccatcac agatgacata tgatcttcag 1400
 ctgacaaatt tgttgaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390

<211> 146

<212> PRT

<213> Homo sapiens

<400> 390

Met	Ser	Arg	Ser	Arg	Leu	Phe	Ser	Val	Thr	Ser	Ala	Ile	Ser	Thr
1				5					10					15

Ile	Gly	Ile	Leu	Cys	Leu	Pro	Leu	Phe	Gln	Leu	Val	Leu	Ser	Asp	
				20					25					30	
Leu	Pro	Cys	Glu	Glu	Asp	Glu	Met	Cys	Val	Asn	Tyr	Asn	Asp	Gln	
			35						40					45	
His	Pro	Asn	Gly	Trp	Tyr	Ile	Trp	Ile	Leu	Leu	Leu	Leu	Val	Leu	
			50						55					60	
Val	Ala	Ala	Leu	Leu	Cys	Gly	Ala	Val	Val	Leu	Cys	Leu	Gln	Cys	
			65						70					75	
Trp	Leu	Arg	Arg	Pro	Arg	Ile	Asp	Ser	His	Arg	Arg	Thr	Met	Ala	
				80					85					90	
Val	Phe	Ala	Val	Gly	Asp	Leu	Asp	Ser	Ile	Tyr	Gly	Thr	Glu	Ala	
			95						100					105	
Ala	Val	Ser	Pro	Thr	Val	Gly	Ile	His	Leu	Gln	Thr	Gln	Thr	Pro	
				110					115					120	
Asp	Leu	Tyr	Pro	Val	Pro	Ala	Pro	Cys	Phe	Gly	Pro	Leu	Gly	Ser	
				125					130					135	
Pro	Pro	Pro	Tyr	Glu	Glu	Ile	Val	Lys	Thr	Thr					
				140					145						

<210> 391
 <211> 26
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

 <400> 391
 cttttcagtg tcacctcagc gatctc 26

 <210> 392
 <211> 23
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

 <400> 392
 ccaaaacatg gagcaggaac agg 23

 <210> 393
 <211> 47
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 393
ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 394
gagcggagta aaatctccac aagctgggaa caaacctcgt cccaactccc 50
accacccggc gtttctccag ctcatctcct ggtgactga gtttaataagag tggatacaac 100
gacgcagctg acgcccgtt attagctctc gctgcgtcgc cccggctcag 150
aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200
tctcttctac tttgggagag agagaaagtc agatgccctt tttaaactcc 250
ctcttcaaaa ctcatctcct ggtgactga gtttaataagag tggatacaac 300
cttgctgaag atgaagaata tacaatattg aggatatttt tttctttttt 350
ttttcaagtc ttgatttgtg gcttacctca agttaccatt tttcagtcaa 400
gtctgtttgt ttgcttcttc agaaatgttt tttacaatct caagaaaaaa 450
tatgtcccag aaattgagtt tactgttget tgtatttggga ctcatgtggg 500
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<210> 395

<211> 140

<212> PRT

<213> Homo sapiens

<400> 395

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20 25 30
His Tyr Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu
35 40 45
Arg Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu
50 55 60
Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser
65 70 75
Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu Leu
80 85 90
Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp
95 100 105
Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr
110 115 120
Ser Gly Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val
125 130 135
Ser Gly Ser Ile Arg
140

<210> 396
<211> 2639
<212> DNA
<213> Homo sapiens

<400> 396
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accttcggcc ttttcgacag cttcagcctg actcgggtgg attgtagcgg 200
cctgggcccc cacatcatgc cggtgcccat ccctctggac acagcccact 250
tggacctgtc ctccaaccgg ctggagatgg tgaatgagtc ggtggtggcg 300
gggcccgggt acacgacgtt ggctggcctg gatctcagcc acaacctgct 350
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agctcaccctc tgagcgacgt gaaccttagc cacaaccagc tccgggaggt 500
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 aagctgggca tcagtggcca catgggcac aggggctggc cccacagaga 2500
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2639

<210> 397

<211> 353

<212> PRT

<213> Homo sapiens

<400> 397

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Thr	Thr	Arg	Pro	Cys	Phe	Pro	Gly	Cys	Gln	Cys	Glu	Val	Glu	Thr
				20					25					30
Phe	Gly	Leu	Phe	Asp	Ser	Phe	Ser	Leu	Thr	Arg	Val	Asp	Cys	Ser
				35					40					45
Gly	Leu	Gly	Pro	His	Ile	Met	Pro	Val	Pro	Ile	Pro	Leu	Asp	Thr
				50					55					60
Ala	His	Leu	Asp	Leu	Ser	Ser	Asn	Arg	Leu	Glu	Met	Val	Asn	Glu
				65					70					75
Ser	Val	Leu	Ala	Gly	Pro	Gly	Tyr	Thr	Thr	Leu	Ala	Gly	Leu	Asp
				80					85					90
Leu	Ser	His	Asn	Leu	Leu	Thr	Ser	Ile	Ser	Pro	Thr	Ala	Phe	Ser
				95					100					105
Arg	Leu	Arg	Tyr	Leu	Glu	Ser	Leu	Asp	Leu	Ser	His	Asn	Gly	Leu
				110					115					120
Thr	Ala	Leu	Pro	Ala	Glu	Ser	Phe	Thr	Ser	Ser	Pro	Leu	Ser	Asp
				125					130					135
Val	Asn	Leu	Ser	His	Asn	Gln	Leu	Arg	Glu	Val	Ser	Val	Ser	Ala
				140					145					150

Phe	Thr	Thr	His	Ser	Gln	Gly	Arg	Ala	Leu	His	Val	Asp	Leu	Ser	155	160	165
His	Asn	Leu	Ile	His	Arg	Leu	Val	Pro	His	Pro	Thr	Arg	Ala	Gly	170	175	180
Leu	Pro	Ala	Pro	Thr	Ile	Gln	Ser	Leu	Asn	Leu	Ala	Trp	Asn	Arg	185	190	195
Leu	His	Ala	Val	Pro	Asn	Leu	Arg	Asp	Leu	Pro	Leu	Arg	Tyr	Leu	200	205	210
Ser	Leu	Asp	Gly	Asn	Pro	Leu	Ala	Val	Ile	Gly	Pro	Gly	Ala	Phe	215	220	225
Ala	Gly	Leu	Gly	Gly	Leu	Thr	His	Leu	Ser	Leu	Ala	Ser	Leu	Gln	230	235	240
Arg	Leu	Pro	Glu	Leu	Ala	Pro	Ser	Gly	Phe	Arg	Glu	Leu	Pro	Gly	245	250	255
Leu	Gln	Val	Leu	Asp	Leu	Ser	Gly	Asn	Pro	Lys	Leu	Asn	Trp	Ala	260	265	270
Gly	Ala	Glu	Val	Phe	Ser	Gly	Leu	Ser	Ser	Leu	Gln	Glu	Leu	Asp	275	280	285
Leu	Ser	Gly	Thr	Asn	Leu	Val	Pro	Leu	Pro	Glu	Ala	Leu	Leu	Leu	290	295	300
His	Leu	Pro	Ala	Leu	Gln	Ser	Val	Ser	Val	Gly	Gln	Asp	Val	Arg	305	310	315
Cys	Arg	Arg	Leu	Val	Arg	Glu	Gly	Thr	Tyr	Pro	Arg	Arg	Pro	Gly	320	325	330
Ser	Ser	Pro	Lys	Val	Pro	Leu	His	Cys	Val	Asp	Thr	Arg	Glu	Ser	335	340	345
Ala	Ala	Arg	Gly	Pro	Thr	Ile	Leu								350		

<210> 398
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 398
 ccctgccagc cgagagcttc acc 23

<210> 399
 <211> 23
 <212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400

caacccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

gatggcgcag ccacagcttc tgtgagattc gatttctccc cagttcccct 50

gtgggtctga ggggaccaga agggtagct acgttggtt tctggaaggg 100

gaggctatat gcgtcaattc cccaaaacaa gttttgacat ttcccctgaa 150

atgtcattct ctatctattc actgcaagt cctgctgttc caggccttac 200

ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250

cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350

tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400

ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450

ttgggaagct gtgtgatcgc cacaaacctt caggaaatac gaaatggatt 500

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ccaattcctt tcttaccatc aagaaggacc tccggctctc tcatgccac 750

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ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500
aatcctacac ggccagcatg tttttctaca aataaagttt tctttgcata 1550
ccaaaaaaaa aaaaaaaaaa a 1571

<210> 402
<211> 261
<212> PRT
<213> Homo sapiens

<400> 402
Met Arg Gln Phe Pro Lys Thr Ser Phe Asp Ile Ser Pro Glu Met
1 5 10 15
Ser Phe Ser Ile Tyr Ser Leu Gln Val Pro Ala Val Pro Gly Leu
20 25 30
Thr Cys Trp Ala Leu Thr Ala Glu Pro Gly Trp Gly Gln Asn Lys
35 40 45
Gly Ala Thr Thr Cys Ala Thr Asn Ser His Ser Asp Ser Glu Leu
50 55 60
Arg Pro Glu Ile Phe Ser Ser Arg Glu Ala Trp Gln Phe Phe Leu
65 70 75
Leu Leu Trp Ser Pro Asp Phe Arg Pro Lys Met Lys Ala Ser Ser
80 85 90

Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr	
				95					100					105	
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile	
				110					115					120	
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg	
				125					130					135	
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu	
				140					145					150	
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys	
				155					160					165	
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe	
				170					175					180	
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser	
				185					190					195	
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu	
				200					205					210	
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys	
				215					220					225	
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln	
				230					235					240	
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln	
				245					250					255	
Trp	Met	Glu	Glu	Thr	Glu										
				260											

<210> 403

<211> 28

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-28

<223> Synthetic construct.

<400> 403

ctcctgtggt ctccagattt caggccta 28

<210> 404

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 404
agtcctcctt aagattctga tgtcaa 26

<210> 405
<211> 998
<212> DNA
<213> Homo sapiens

<400> 405
ccgttatcgt cttgcgctac tgctgaatgt ccgtcccgga ggaggaggag 50
aggctttttgc cgctgacca gagatggccc cgagcgagca aattcctact 100
gtccggctgc gcggctaccg tggccgagct agcaaccttt cccctggatc 150
tcacaaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200
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tccccttttg aaatcagtca ttggagggat gatggctggg gttattggcc 450
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ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550
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gctttttacc atcttggctg agaatgacct cttggtcaat ggtgttctgg 950
cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406
<211> 323
<212> PRT
<213> Homo sapiens

<400> 406
Met Ser Val Pro Glu Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln
1 5 10 15

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				20					25					30	
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr	
				35					40					45	
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp	
				50					55					60	
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala	
				65					70					75	
Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly	
				80					85					90	
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg	
				95					100					105	
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser	
				110					115					120	
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met	
				125					130					135	
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu	
				140					145					150	
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly	
				155					160					165	
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile	
				170					175					180	
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro	
				185					190					195	
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr	
				200					205					210	
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu	
				215					220					225	
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu	
				230					235					240	
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg	
				245					250					255	
Ile	Met	Asn	Gln	Pro	Arg	Asp	Lys	Gln	Gly	Arg	Gly	Leu	Leu	Tyr	
				260					265					270	
Lys	Ser	Ser	Thr	Asp	Cys	Leu	Ile	Gln	Ala	Val	Gln	Gly	Glu	Gly	
				275					280					285	
Phe	Met	Ser	Leu	Tyr	Lys	Gly	Phe	Leu	Pro	Ser	Trp	Leu	Arg	Met	
				290					295					300	
Thr	Pro	Trp	Ser	Met	Val	Phe	Trp	Leu	Thr	Tyr	Glu	Lys	Ile	Arg	

305

310

315

Glu Met Ser Gly Val Ser Pro Phe
320

<210> 407
<211> 31
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-31
<223> Synthetic construct.

<400> 407
cgcggtatccc gttatcgtct tgcgctactg c 31

<210> 408
<211> 34
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-34
<223> Synthetic construct.

<400> 408
gcggaattct taaaatggac tgactccact catc 34

<210> 409
<211> 1487
<212> DNA
<213> Homo sapiens

<400> 409
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cagcatttaa tgaaaaattt atgcttaaga agtaaaaatg gcaggcttcc 150
tagataattt tcgttggcca gaatgtgaat gtattgactg gagtgagaga 200
agaaatgctg tggcatctgt tgtcgcaggt atattgtttt ttacaggctg 250
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ctgttttagga agaacagggtg ctcgagtttg gcttttcatt ggtttcatgt 450
tgatgtttgg gtcacttatt gcttccatgt ggattctttt tgggtgcatat 500
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380

TopRefSeq = 93847007

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<210> 410

<211> 158

<212> PRT

<213> Homo sapiens

<400> 410

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Gly	Ile	Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Met	Ile	Asp	Ala	Ala
				35					40					45
Val	Val	Tyr	Pro	Lys	Pro	Glu	Gln	Leu	Asn	His	Ala	Phe	His	Thr
				50					55					60
Cys	Gly	Val	Phe	Ser	Thr	Leu	Ala	Phe	Phe	Met	Ile	Asn	Ala	Val
				65					70					75

Ser	Asn	Ala	Gln	Val	Arg	Gly	Asp	Ser	Tyr	Glu	Ser	Gly	Cys	Leu
				80					85					90
Gly	Arg	Thr	Gly	Ala	Arg	Val	Trp	Leu	Phe	Ile	Gly	Phe	Met	Leu
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Met	Phe	Gly	Ser	Leu	Ile	Ala	Ser	Met	Trp	Ile	Leu	Phe	Gly	Ala
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Tyr	Val	Thr	Gln	Asn	Thr	Asp	Val	Tyr	Pro	Gly	Leu	Ala	Val	Phe
				125					130					135
Phe	Gln	Asn	Ala	Leu	Ile	Phe	Phe	Ser	Thr	Leu	Ile	Tyr	Lys	Phe
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 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 411
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<210> 412
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 <212> DNA
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<220>
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 <222> 1-20
 <223> Synthetic construct.

<400> 412
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<210> 413
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<220>
 <221> Artificial Sequence
 <222> 1-40
 <223> Synthetic construct.

<400> 413
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<210> 414

<211> 1337
<212> DNA
<213> Homo sapiens

<400> 414
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gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200
gggacctacg gcacctgctg gaccacctcg ccttctccat cgaagcaggg 250
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<210> 415
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 415

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Met	Lys	Thr	Ile	Arg	Leu	Pro	Arg	Trp	Leu	Ala	Ala	Ser	Pro	Thr	35	40	45	
Lys	Glu	Ile	Gln	Val	Lys	Lys	Tyr	Lys	Cys	Gly	Leu	Ile	Lys	Pro	50	55	60	
Cys	Pro	Ala	Asn	Tyr	Phe	Ala	Phe	Lys	Ile	Cys	Ser	Gly	Ala	Ala	65	70	75	
Asn	Val	Val	Gly	Pro	Thr	Met	Cys	Phe	Glu	Asp	Arg	Met	Ile	Met	80	85	90	
Ser	Pro	Val	Lys	Asn	Asn	Val	Gly	Arg	Gly	Leu	Asn	Ile	Ala	Leu	95	100	105	
Val	Asn	Gly	Thr	Thr	Gly	Ala	Val	Leu	Gly	Gln	Lys	Ala	Phe	Asp	110	115	120	
Met	Tyr	Ser	Gly	Asp	Val	Met	His	Leu	Val	Lys	Phe	Leu	Lys	Glu	125	130	135	
Ile	Pro	Gly	Gly	Ala	Leu	Val	Leu	Val	Ala	Ser	Tyr	Asp	Asp	Pro	140	145	150	
Gly	Thr	Lys	Met	Asn	Asp	Glu	Ser	Arg	Lys	Leu	Phe	Ser	Asp	Leu	155	160	165	
Gly	Ser	Ser	Tyr	Ala	Lys	Gln	Leu	Gly	Phe	Arg	Asp	Ser	Trp	Val	170	175	180	
Phe	Ile	Gly	Ala	Lys	Asp	Leu	Arg	Gly	Lys	Ser	Pro	Phe	Glu	Gln	185	190	195	
Phe	Leu	Lys	Asn	Ser	Pro	Asp	Thr	Asn	Lys	Tyr	Glu	Gly	Trp	Pro	200	205	210	
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<210> 416
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

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<222> 1-21
<223> Synthetic construct.

<400> 416
gccatagtca cgacatggat g 21

<210> 417
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 417
ggatggccag agctgctg 18

<210> 418
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.

<400> 418
aaagtacaag tgtggcctca tcaagc 26

<210> 419
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 419
tctgactcct aagtcaggca ggag 24

<210> 420
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 420
attctctcca cagacagctg gttc 24

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<210> 421
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 421
gtacaagtgt ggcctcatca agccctgccc agccaactac tttgcg 46

<210> 422
<211> 1701
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1528
<223> unknown base

<400> 422
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cacgccagga gtcgctcgc tctctctctc tctctctcac tctccctcc 200
ctctctctct gctgtccta gtcctctagt cctcaaattc ccagtccct 250
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cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450
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cactggggtc agaaaggatc ccagggggg tcagaacacc agatcaacag 650
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atgacagctt gagtgaggct gctgagaggc ctcagggcct ggctgtcctg 750
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tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850

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t 1701

<210> 423
<211> 337
<212> PRT
<213> Homo sapiens

<400> 423
Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala
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Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln
20 25 30
Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln
35 40 45
Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp
50 55 60
Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu
65 70 75
Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 424
 gtaaagtcgc tggccagc 18

<210> 425
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 425
 cccgatctgc ctgctgta 18

<210> 426
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 426
 ctgcactgta tggccattat tgtg 24

<210> 427
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 427
 cagaaacca tgatacccta ctgaacaccg aatcccctgg aagcc 45

<210> 428
 <211> 1073
 <212> DNA
 <213> Homo sapiens

<400> 428
 aatttttcac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50
 acattttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100
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aacctgcttt gggactccct ccacaaaaac tggctccgga tcagggaaca 200
 ctaccaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250
 accattaaca cagatgctca cactggggcc agatctgcat ctgttaaata 300
 ctgctgcagg aatgacacct ggtaccaga cccaccatt gaccctggga 350
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 cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450
 aaatcttcac gagcctcatc atccattcct tgttcccggg aggcattcctg 500
 cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550
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 gcctcccaac tcccagtggc acagatgacg actttgcagt gaccaccct 650
 gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaatc 700
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 gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850
 gaaaatattc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900
 cttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050
 aaaaaaaaaa aaaaaaaaaa aaa 1073

<210> 429
 <211> 209
 <212> PRT
 <213> Homo sapiens

<400> 429
 Met Arg Ser Thr Ile Leu Leu Phe Cys Leu Leu Gly Ser Thr Arg
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 Ser Leu Pro Gln Leu Lys Pro Ala Leu Gly Leu Pro Pro Thr Lys
 20 25 30
 Leu Ala Pro Asp Gln Gly Thr Leu Pro Asn Gln Gln Gln Ser Asn
 35 40 45
 Gln Val Phe Pro Ser Leu Ser Leu Ile Pro Leu Thr Gln Met Leu
 50 55 60
 Thr Leu Gly Pro Asp Leu His Leu Leu Asn Pro Ala Ala Gly Met
 65 70 75

Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn	80	85	90
Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr	95	100	105
Gln	Leu	Gly	Ala	Gln	Gly	Thr	Ile	Leu	Ser	Ser	Glu	Glu	Leu	Pro	110	115	120
Gln	Ile	Phe	Thr	Ser	Leu	Ile	Ile	His	Ser	Leu	Phe	Pro	Gly	Gly	125	130	135
Ile	Leu	Pro	Thr	Ser	Gln	Ala	Gly	Ala	Asn	Pro	Asp	Val	Gln	Asp	140	145	150
Gly	Ser	Leu	Pro	Ala	Gly	Gly	Ala	Gly	Val	Asn	Pro	Ala	Thr	Gln	155	160	165
Gly	Thr	Pro	Ala	Gly	Arg	Leu	Pro	Thr	Pro	Ser	Gly	Thr	Asp	Asp	170	175	180
Asp	Phe	Ala	Val	Thr	Thr	Pro	Ala	Gly	Ile	Gln	Arg	Ser	Thr	His	185	190	195
Ala	Ile	Glu	Glu	Ala	Thr	Thr	Glu	Ser	Ala	Asn	Gly	Ile	Gln		200	205	

<210> 430
 <211> 1257
 <212> DNA
 <213> Homo Sapien

<400> 430
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 ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150
 gccccgccgc ctccccgcag cggctccgcg gcctcctgct gctcctgctg 200
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 aaaggcgcag ctccggcaga gggaggtggt ggacctgtat aatggaatgt 300
 gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc 350
 aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400
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 aaaattgcgg agtgtacatt tacaaagatg cgttcaaata gtgctctaag 550
 agttttgttc agtggctcac ttcggctaaa atgcagaaat gcatgctgtc 600
 agcgttggtg tttcacattc aatggagctg aatgttcagg acctcttccc 650

attgaagcta taatttat tttt ggaccaagga agccctgaaa tgaattcaac 700
aattaatatt catcgcaactt cttctgtgga aggactttgt gaaggaattg 750
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ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200
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tccaaca 1257

<210> 431
<211> 243
<212> PRT
<213> Homo Sapien

<400> 431
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20 25 30
Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
35 40 45
Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
50 55 60
Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
65 70 75
Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
80 85 90
Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
95 100 105
Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
110 115 120
Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
125 130 135

Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg
				140					145					150
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu
				155					160					165
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln
				170					175					180
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser
				185					190					195
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp
				200					205					210
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp
				215					220					225
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu
				230					235					240

Leu Pro Lys

<210> 432
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial Sequence

<400> 432
 aggacttgcc ctcaggaa 18

<210> 433
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 433
 cgcaggacag ttgtgaaaat a 21

<210> 434
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 434
 atgacgctcg tccaaggcca c 21

<210> 435

<211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 435
 cccacctgta ccaccatgt 19

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